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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/US95/16733 <b>(22) International Filing Date:</b> 20 December 1995 (20.12.95)  <b>(30) Priority Data:</b> 360,107                      20 December 1994 (20.12.94)      US 470,896                      6 June 1995 (06.06.95)                      US  <b>(71) Applicants:</b> DUKE UNIVERSITY [US/US]; Erwin Road, Durham, NC 27706 (US). TRIMERIS INC. [US/US]; 4727 University Drive, Durham, NC 27707-3438 (US).  <b>(72) Inventors:</b> BOLOGNESI, Dani, P.; 17 Harvey Place, Durham, NC 27705 (US). MATTHEWS, Thomas, J.; 5906 Newhall Road, Durham, NC 27713 (US). WILD, Cart, T.; 1702 B Vista Street, Durham, NC 27701 (US). BARNEY, Shawn, O'Lin; 106 Branchway Road, Cary, NC 27502 (US). LAMBERT, Dennis, M.; 101 Centerville Court, Cary, NC 27513 (US). PETTEWAY, Stephen, R., Jr.; 203 Le Gault Drive, Cary, NC 27513 (US). LANGLOIS, Alphonse, J.; 1720 Vista Street, Durham, NC 27701 (US).  <b>(74) Agents:</b> CORUZZI, Laura, A. et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).		<b>(81) Designated States:</b> AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, LS, MW, SD, SZ, UG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION		
<b>(57) Abstract</b>  The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID: 1) peptide corresponding to amino acids 638 to 673 of the HIV-1 LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.		



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**METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION**

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a  
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government  
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

**1. INTRODUCTION**

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,  
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4<sup>+</sup> cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178  
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids  
30 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion  
35 capability, antiviral activity, or the ability to



modulat intracellular processes inv lving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4<sup>+</sup> cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

## 2. BACKGROUND OF THE INVENTION

### 2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.



Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

5 Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell  
10 death.

## 2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly  
15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of  
20 each of these types. Infection of human CD-4<sup>+</sup> T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

25 HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and  
30  
35



replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I, -II, -III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4<sup>+</sup> cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4<sup>+</sup> receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4<sup>+</sup> cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.



### 2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the  
5 successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991,  
10 FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been  
15 developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989,  
20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs  
25 which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4<sup>+</sup> T-cells by some  
30 HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,  
35



recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5       The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and  
10       drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15       Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,  
20       these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.  
25       See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30       Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

35



### 3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1<sub>LAI</sub>), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and/or organisms other than HIV-1<sub>LAI</sub>. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the



DP107 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and organisms other than HIV-1<sub>LAI</sub>. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4<sup>+</sup> cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that



th peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.



Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion (*i.e.*,  
5 syncytial formation) and infection of CD-4<sup>+</sup> cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery  
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and  
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral  
25 sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the  
30 invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.



### 3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with  
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino  
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as  
15 follows:

A (alanine)  
R (arginine)  
N (asparagine)  
D (aspartic acid)  
C (cysteine)  
20 Q (glutamine)  
E (glutamic acid)  
G (glycine)  
H (histidine)  
I (isoleucine)  
L (leucine)  
K (lysine)  
M (methionine)  
25 F (phenylalanine)  
P (proline)  
S (serine)  
T (threonine)  
W (tryptophan)  
Y (tyrosine)  
V (valine)

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#### 4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV<sub>LAI</sub>; DP178 homologs derived from HIV-1<sub>SP2</sub> (DP-185; SEQ ID:3), HIV-1<sub>RF</sub> (SEQ ID:4), and HIV-1<sub>MOI</sub> (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2<sub>red</sub> (SEQ ID:6) and HIV-2<sub>NDZ</sub> (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC<sub>50</sub> refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC<sub>50</sub>: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.



4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1<sub>SP2</sub> isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5       FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

      FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell  
10 proliferation data is shown.

      FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter  
15 P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and  
Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM.  
20 The proteins are more fully described, below, in Section 8.1.1.

      FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

      FIG. 9. Abrogation of DP178 anti-HIV activity.  
25 Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PΔ178.

      FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

30       FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common  
35



features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended  $\alpha$ -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be



the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

5 FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

10 FIG. 20. Search results for HIV-1 (BRU isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIP; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program  
15 designed to search for such peptide regions). Asterisk (\*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and  
20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations  
25 are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations  
30 are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations  
35 are as in FIG. 20.



FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

10 FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

15 FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20        "-", negative antiviral activity;  
      "+/-", antiviral activity at greater than 100µg/ml;  
      "+", antiviral activity at between 50-100µg/ml;  
      "++", antiviral activity at between 20-50µg/ml;  
      "+++", antiviral activity at between 1-20µg/ml;  
25        "++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

30        "-", no helicity;  
      "+", 25-50% helicity;  
      "++", 50-75% helicity;  
      "+++" 75-100% helicity.

35        IC<sub>50</sub> refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures



c ntaining no peptide.  $IC_{50}$  values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as  
5 in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG.  
10 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG.  
15 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were  
20 obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as  
25 in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dim rization domain, as defined  
35



by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

5 FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

10 FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for *Pseudomonas aeruginosa*, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

15 FIG. 38. Motif search results for *Neisseria gonorrhoeae* fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for *Hemophilus influenzae* fimbrial protein. Sequence search designations are as in FIG. 20.

20 FIG. 40. Motif search results for *Staphylococcus aureus*, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

25 FIG. 41. Motif search results for *Staphylococcus aureus* enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for *Staphylococcus aureus* enterotoxin A. Sequence search designations are as in FIG. 20.

30 FIG. 43. Motif search results for *Escherichia coli*, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The column to the immediate right of the test peptide name



indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself.  $IC_{50}$  is as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data.  $IC_{50}$  as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The



length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

## 5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate



intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, *infra*. In the HIV protein, gp41, DP178 corresponds to a putative  $\alpha$ -helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal  $\alpha$ -helix motif of gp41 (*i.e.*, the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (*i.e.*, the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal  $\alpha$ -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

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On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107



peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, *infra*, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

#### 5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1<sub>LA1</sub> isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)



In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below.

Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ( $-NH_2$ ) and "Z" may represent a carboxyl ( $-COOH$ ) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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**TABLE I**  
**DP178 (SEQ ID:1) CARBOXY TRUNCATIONS**

X-YTS-Z  
 X-YTSL-Z  
 X-YTSLI-Z  
 X-YTSLIH-Z  
 5 X-YTSLIHS-Z  
 X-YTSLIHSL-Z  
 X-YTSLIHSLI-Z  
 X-YTSLIHSLIE-Z  
 X-YTSLIHSLIEE-Z  
 X-YTSLIHSLIEES-Z  
 X-YTSLIHSLIEESQ-Z  
 10 X-YTSLIHSLIEESQN-Z  
 X-YTSLIHSLIEESQNNQ-Z  
 X-YTSLIHSLIEESQNNQQ-Z  
 X-YTSLIHSLIEESQNNQQE-Z  
 X-YTSLIHSLIEESQNNQQEK-Z  
 X-YTSLIHSLIEESQNNQQEKN-Z  
 X-YTSLIHSLIEESQNNQQEKNE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQ-Z  
 15 X-YTSLIHSLIEESQNNQQEKNEQE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELD-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDK-Z  
 20 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWN-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWNW-Z  
 25 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWNWF-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE IA  
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
5	X-SLWNWF-Z
	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
	X-LLELDKWASLWNWF-Z
10	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
	X-QEKNEQELLELDKWASLWNWF-Z
15	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQQEKNEQELLELDKWASLWNWF-Z
	X-QNQQEKNEQELLELDKWASLWNWF-Z
	X-SQNQQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
20	X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.



Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

## 5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein, as shown here:

NH<sub>2</sub>-NNLLRAIEAQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH  
(SEQ ID:25)

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes



inv lving coiled-c il peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ( $-NH_2$ ) and "Z" may represent a carboxyl ( $-COOH$ ) group. Alternatively, "X" may represent a hydrophobic group, including but not  
10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or  
15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred  
20 "X" or "Z" macromolecular group is a peptide group.

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TABLE II  
DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

	X>NNL-Z
	X>NNLL-Z
	X>NNLLR-Z
5	X>NNLLRA-Z
	X>NNLLRAI-Z
	X>NNLLRAIE-Z
	X>NNLLRAIEA-Z
	X>NNLLRAIEAQ-Z
	X>NNLLRAIEAQQ-Z
	X>NNLLRAIEAQQH-Z
10	X>NNLLRAIEAQQHL-Z
	X>NNLLRAIEAQQHLL-Z
	X>NNLLRAIEAQQHLLQ-Z
	X>NNLLRAIEAQQHLLQL-Z
	X>NNLLRAIEAQQHLLQLT-Z
	X>NNLLRAIEAQQHLLQLTV-Z
	X>NNLLRAIEAQQHLLQLTVW-Z
	X>NNLLRAIEAQQHLLQLTVWQ-Z
15	X>NNLLRAIEAQQHLLQLTVWQI-Z
	X>NNLLRAIEAQQHLLQLTVWQIK-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQ-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQL-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQ-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQA-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z
20	X>NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z
25	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.
- 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE IIA  
DP178 (SEQ ID:25) AMINO TRUNCATIONS

	X-KDQ-	Z
	X-LKDQ-	Z
5	X-YLKDQ-	Z
	X-RYLKDQ-	Z
	X-ERYLKDQ-	Z
	X-VERYLKDQ-	Z
	X-AVERYLKDQ-	Z
	X-LAVERYLKDQ-	Z
	X-ILAVERYLKDQ-	Z
10	X-RILAVERYLKDQ-	Z
	X-ARILAVERYLKDQ-	Z
	X-QARILAVERYLKDQ-	Z
	X-LQARILAVERYLKDQ-	Z
	X-QLQARILAVERYLKDQ-	Z
	X-KQLQARILAVERYLKDQ-	Z
	X-IKQLQARILAVERYLKDQ-	Z
	X-QIKQLQARILAVERYLKDQ-	Z
15	X-WQIKQLQARILAVERYLKDQ-	Z
	X-VWQIKQLQARILAVERYLKDQ-	Z
	X-TVWQIKQLQARILAVERYLKDQ-	Z
	X-LTVWQIKQLQARILAVERYLKDQ-	Z
	X-QLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLQLTVWQIKQLQARILAVERYLKDQ-	Z
20	X-HLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
25	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.



Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

### 5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1<sub>LAI</sub> enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the



ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (*i.e.*, other than HIV-1<sub>LAI</sub>) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41 peptide region of other (*i.e.*, non HIV-1<sub>LAI</sub>) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH<sub>2</sub>-YTNTIYTLLEESQNQQEKNEQEELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH<sub>2</sub>-YTGIIYNLLEESQNQQEKNEQEELLELDKWANLWNWF-COOH (SEQ ID:4);

NH<sub>2</sub>-YTSLIYSLLEKSQIQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1<sub>SF2</sub>, HIV-1<sub>RF</sub>, and HIV-1<sub>MN</sub> isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such



DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the  
5 analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41  
10 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178  
15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2<sub>NIH2</sub> isolate has the 36 amino acid  
20 sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations  
25 of the HIV-2<sub>NIH2</sub> DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right)  
30 terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-  
35 fluorenylmethoxy-carbonyl (Fmoc) group; or a



c valently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached  
5 macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

10

15

20

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30

35



TABLE IIIHIV-2<sub>ND4Z</sub> DP178 analog carboxy truncati ns.

X-LEA-Z  
 X-LEAN-Z  
 X-LEANI-Z  
 X-LEANIS-Z  
 5 X-LEANISQ-Z  
 X-LEANISQS-Z  
 X-LEANISQSL-Z  
 X-LEANISQSLE-Z  
 X-LEANISQSLEQ-Z  
 X-LEANISQSLEQA-Z  
 X-LEANISQSLEQAAQ-Z  
 10 X-LEANISQSLEQAQI-Z  
 X-LEANISQSLEQAQIQ-Z  
 X-LEANISQSLEQAQIQQ-Z  
 X-LEANISQSLEQAQIQQE-Z  
 X-LEANISQSLEQAQIQQEK-Z  
 X-LEANISQSLEQAQIQQEKN-Z  
 X-LEANISQSLEQAQIQQEKNM-Z  
 X-LEANISQSLEQAQIQQEKNMY-Z  
 15 X-LEANISQSLEQAQIQQEKNMYE-Z  
 X-LEANISQSLEQAQIQQEKNMYEL-Z  
 X-LEANISQSLEQAQIQQEKNMYELQ-Z  
 X-LEANISQSLEQAQIQQEKNMYELQK-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKL-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLN-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z  
 20 X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z  
 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE IV

HIV-2<sub>NDH2</sub> DP178 analog amino truncations.

	X-NWL-2
	X-TNWL-2
	X-FTNWL-2
5	X-VFTNWL-2
	X-DVFTNWL-2
	X-WDVFTNWL-2
	X-SWDVFTNWL-2
	X-NSWDVFTNWL-2
	X-LNSWDVFTNWL-2
	X-KLNSWDVFTNWL-2
	X-QKLNSWDVFTNWL-2
10	X-LQKLNSWDVFTNWL-2
	X-ELQKLNSWDVFTNWL-2
	X-YELQKLNSWDVFTNWL-2
	X-MYELQKLNSWDVFTNWL-2
	X-NMYELQKLNSWDVFTNWL-2
	X-KNMYELQKLNSWDVFTNWL-2
	X-EKNMYELQKLNSWDVFTNWL-2
15	X-QEKNMYELQKLNSWDVFTNWL-2
	X-QQEKNMYELQKLNSWDVFTNWL-2
	X-IQQEKNMYELQKLNSWDVFTNWL-2
	X-QIQQEKNMYELQKLNSWDVFTNWL-2
	X-AQIQQEKNMYELQKLNSWDVFTNWL-2
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-2
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-2

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for



identifying protein regions analog us to DP107 r  
DP178.

Specifically, analysis of HIV-1 gp160 (containing  
both gp120 and gp41) using the Lupas algorithm does  
not identify the coiled-coil region within DP107. It  
5 does, however, identify a region within DP178  
beginning eight amino acids N-terminal to the start of  
DP178 and ending eight amino acids from the C-  
terminus. The DP107 peptide has been shown  
experimentally to form a stable coiled coil. A search  
10 based on the Lupas search algorithm, therefore, would  
not have identified the DP107 coiled-coil region.  
Conversely, the Lupas algorithm identified the DP178  
region as a potential coiled-coil motif. However, the  
peptide derived from the DP178 region failed to form a  
15 coiled coil in solution.

A possible explanation for the inability of the  
Lupas search algorithm to accurately identify coiled-  
coil sequences within the HIV-1 TM, is that the Lupas  
algorithm is based on the structure of coiled coils  
20 from proteins that are not structurally or  
functionally similar to the TM proteins of viruses,  
antiviral peptides (e.g. DP107 and DP178) of which are  
an object of this invention.

The computer search strategy of the invention, as  
25 demonstrated in the Examples presented below, in  
Sections 9 through 16 and 19 through 25, successfully  
identifies regions of proteins similar to DP107 or  
DP178. This search strategy was designed to be used  
with a commercially-available sequence database  
30 package, preferably PC/Gene.

A series of search motifs, the 107x178x4,  
ALLMOTI5 and PLZIP motifs, were designed and  
engineered to range in stringency from strict to  
broad, as discussed in this Section and in Section 9,  
35 with 107x178x4 being preferred. The sequences



identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are  
 5 intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first  
 10 position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by  
 15 brackets, i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed  
 20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g., a (2) means "for the next two heptad amino acid positions".

25 The ALLMOTI5 is written as follows:

{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
 {CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
 {CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
 {CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
 {CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-

30 Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth  
 35 heptad position (D), any amino acid residue except C,



D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for



four consecutive heptad repeats (thus the repeat of  
th first line four times), meaning that it search s  
for 28-mer sized peptides. It may also be designed to  
search for 35-mers, by repeating the initial motif  
five times. With respect to the 107x178x4 motif, a  
5 28-mer search is preferred.

Those viral (non-bacteriophage) sequences  
identified via such a 107x178x4 motif are listed in  
Table VI, below, at the end of this Section, with  
those viral (non-bacteriophage) sequences listed in  
10 Table VII, below at the end of this Section, being  
preferred.

The 107x178x4 search motif was also utilized to  
identify non-viral procaryotic protein sequences, as  
listed in Table VIII, below, at the end of this  
15 Section. Further, this search motif was used to  
reveal a number of human proteins. The results of  
this human protein 107x178x4 search is listed in Table  
IX, below, at the end of this Section. The sequences  
listed in Tables VIII and IX, therefore, reveal  
20 peptides which may be useful as antifusogenic  
compounds or in the identification of antifusogenic  
compounds, and are intended to be within the scope of  
the invention.

The PLZIP series of motifs are as listed in FIG.  
25 19. These motifs are designed to identify leucine  
zipper coiled-coil like heptads wherein at least one  
proline residue is present at some predefined distance  
N-terminal to the repeat. These PLZIP motifs find  
regions of proteins with similarities to HIV-1 DP178  
30 generally located just N-terminal to the transmembrane  
anchor. These motifs may be translated according to  
the same convention described above. Each line  
depicted in FIG. 19 represents a single, complete  
search motif. "X" in these motifs refers to any amino  
35 acid residue. In instances wherein a motif contains



two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

5       Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists  
10       viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table  
15       XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are  
20       intended to be within the scope of the invention.

      The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify  
25       substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-  
30       measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

      The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178,  
35       above, in Section 5.1. For example, these peptides



may include any of the additional amin -terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5 Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions  
10 and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory  
20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX  
25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and  
30 Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped  
35 according to the specific virus which they inhibit,



including respiratory syncytial virus, human  
parainfluenza virus 3, simian immunodeficiency virus  
and measles virus.

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TABLE V

ALLMOT15 SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS



[illegible]



PGENE	ALLNOTES	ABEA1	ABEA2	ABEA3	ABEA4	ABEA5	ABEA6	ABEA7	ABEA8	ABEA9	ABEA10	ABEA11	ABEA12	ABEA13	ABEA14	ABEA15	ABEA16	ABEA17	ABEA18	ABEA19	ABEA20	ABEA21	ABEA22	ABEA23	ABEA24	ABEA25	ABEA26	ABEA27	ABEA28	ABEA29	ABEA30	ABEA31	ABEA32	ABEA33	ABEA34	ABEA35	ABEA36	ABEA37	ABEA38	ABEA39	ABEA40	ABEA41	ABEA42	ABEA43	ABEA44	ABEA45	ABEA46	ABEA47	ABEA48	ABEA49	ABEA50	ABEA51	ABEA52	ABEA53	ABEA54	ABEA55	ABEA56	ABEA57	ABEA58	ABEA59	ABEA60	ABEA61	ABEA62	ABEA63	ABEA64	ABEA65	ABEA66	ABEA67	ABEA68	ABEA69	ABEA70	ABEA71	ABEA72	ABEA73	ABEA74	ABEA75	ABEA76	ABEA77	ABEA78	ABEA79	ABEA80	ABEA81	ABEA82	ABEA83	ABEA84	ABEA85	ABEA86	ABEA87	ABEA88	ABEA89	ABEA90	ABEA91	ABEA92	ABEA93	ABEA94	ABEA95	ABEA96	ABEA97	ABEA98	ABEA99	ABEA100	ABEA101	ABEA102	ABEA103	ABEA104	ABEA105	ABEA106	ABEA107	ABEA108	ABEA109	ABEA110	ABEA111	ABEA112	ABEA113	ABEA114	ABEA115	ABEA116	ABEA117	ABEA118	ABEA119	ABEA120	ABEA121	ABEA122	ABEA123	ABEA124	ABEA125	ABEA126	ABEA127	ABEA128	ABEA129	ABEA130	ABEA131	ABEA132	ABEA133	ABEA134	ABEA135	ABEA136	ABEA137	ABEA138	ABEA139	ABEA140	ABEA141	ABEA142	ABEA143	ABEA144	ABEA145	ABEA146	ABEA147	ABEA148	ABEA149	ABEA150	ABEA151	ABEA152	ABEA153	ABEA154	ABEA155	ABEA156	ABEA157	ABEA158	ABEA159	ABEA160	ABEA161	ABEA162	ABEA163	ABEA164	ABEA165	ABEA166	ABEA167	ABEA168	ABEA169	ABEA170	ABEA171	ABEA172	ABEA173	ABEA174	ABEA175	ABEA176	ABEA177	ABEA178	ABEA179	ABEA180	ABEA181	ABEA182	ABEA183	ABEA184	ABEA185	ABEA186	ABEA187	ABEA188	ABEA189	ABEA190	ABEA191	ABEA192	ABEA193	ABEA194	ABEA195	ABEA196	ABEA197	ABEA198	ABEA199	ABEA200	ABEA201	ABEA202	ABEA203	ABEA204	ABEA205	ABEA206	ABEA207	ABEA208	ABEA209	ABEA210	ABEA211	ABEA212	ABEA213	ABEA214	ABEA215	ABEA216	ABEA217	ABEA218	ABEA219	ABEA220	ABEA221	ABEA222	ABEA223	ABEA224	ABEA225	ABEA226	ABEA227	ABEA228	ABEA229	ABEA230	ABEA231	ABEA232	ABEA233	ABEA234	ABEA235	ABEA236	ABEA237	ABEA238	ABEA239	ABEA240	ABEA241	ABEA242	ABEA243	ABEA244	ABEA245	ABEA246	ABEA247	ABEA248	ABEA249	ABEA250	ABEA251	ABEA252	ABEA253	ABEA254	ABEA255	ABEA256	ABEA257	ABEA258	ABEA259	ABEA260	ABEA261	ABEA262	ABEA263	ABEA264	ABEA265	ABEA266	ABEA267	ABEA268	ABEA269	ABEA270	ABEA271	ABEA272	ABEA273	ABEA274	ABEA275	ABEA276	ABEA277	ABEA278	ABEA279	ABEA280	ABEA281	ABEA282	ABEA283	ABEA284	ABEA285	ABEA286	ABEA287	ABEA288	ABEA289	ABEA290	ABEA291	ABEA292	ABEA293	ABEA294	ABEA295	ABEA296	ABEA297	ABEA298	ABEA299	ABEA300	ABEA301	ABEA302	ABEA303	ABEA304	ABEA305	ABEA306	ABEA307	ABEA308	ABEA309	ABEA310	ABEA311	ABEA312	ABEA313	ABEA314	ABEA315	ABEA316	ABEA317	ABEA318	ABEA319	ABEA320	ABEA321	ABEA322	ABEA323	ABEA324	ABEA325	ABEA326	ABEA327	ABEA328	ABEA329	ABEA330	ABEA331	ABEA332	ABEA333	ABEA334	ABEA335	ABEA336	ABEA337	ABEA338	ABEA339	ABEA340	ABEA341	ABEA342	ABEA343	ABEA344	ABEA345	ABEA346	ABEA347	ABEA348	ABEA349	ABEA350	ABEA351	ABEA352	ABEA353	ABEA354	ABEA355	ABEA356	ABEA357	ABEA358	ABEA359	ABEA360	ABEA361	ABEA362	ABEA363	ABEA364	ABEA365	ABEA366	ABEA367	ABEA368	ABEA369	ABEA370	ABEA371	ABEA372	ABEA373	ABEA374	ABEA375	ABEA376	ABEA377	ABEA378	ABEA379	ABEA380	ABEA381	ABEA382	ABEA383	ABEA384	ABEA385	ABEA386	ABEA387	ABEA388	ABEA389	ABEA390	ABEA391	ABEA392	ABEA393	ABEA394	ABEA395	ABEA396	ABEA397	ABEA398	ABEA399	ABEA400	ABEA401	ABEA402	ABEA403	ABEA404	ABEA405	ABEA406	ABEA407	ABEA408	ABEA409	ABEA410	ABEA411	ABEA412	ABEA413	ABEA414	ABEA415	ABEA416	ABEA417	ABEA418	ABEA419	ABEA420	ABEA421	ABEA422	ABEA423	ABEA424	ABEA425	ABEA426	ABEA427	ABEA428	ABEA429	ABEA430	ABEA431	ABEA432	ABEA433	ABEA434	ABEA435	ABEA436	ABEA437	ABEA438	ABEA439	ABEA440	ABEA441	ABEA442	ABEA443	ABEA444	ABEA445	ABEA446	ABEA447	ABEA448	ABEA449	ABEA450	ABEA451	ABEA452	ABEA453	ABEA454	ABEA455	ABEA456	ABEA457	ABEA458	ABEA459	ABEA460	ABEA461	ABEA462	ABEA463	ABEA464	ABEA465	ABEA466	ABEA467	ABEA468	ABEA469	ABEA470	ABEA471	ABEA472	ABEA473	ABEA474	ABEA475	ABEA476	ABEA477	ABEA478	ABEA479	ABEA480	ABEA481	ABEA482	ABEA483	ABEA484	ABEA485	ABEA486	ABEA487	ABEA488	ABEA489	ABEA490	ABEA491	ABEA492	ABEA493	ABEA494	ABEA495	ABEA496	ABEA497	ABEA498	ABEA499	ABEA500	ABEA501	ABEA502	ABEA503	ABEA504	ABEA505	ABEA506	ABEA507	ABEA508	ABEA509	ABEA510	ABEA511	ABEA512	ABEA513	ABEA514	ABEA515	ABEA516	ABEA517	ABEA518	ABEA519	ABEA520	ABEA521	ABEA522	ABEA523	ABEA524	ABEA525	ABEA526	ABEA527	ABEA528	ABEA529	ABEA530	ABEA531	ABEA532	ABEA533	ABEA534	ABEA535	ABEA536	ABEA537	ABEA538	ABEA539	ABEA540	ABEA541	ABEA542	ABEA543	ABEA544	ABEA545	ABEA546	ABEA547	ABEA548	ABEA549	ABEA550	ABEA551	ABEA552	ABEA553	ABEA554	ABEA555	ABEA556	ABEA557	ABEA558	ABEA559	ABEA560	ABEA561	ABEA562	ABEA563	ABEA564	ABEA565	ABEA566	ABEA567	ABEA568	ABEA569	ABEA570	ABEA571	ABEA572	ABEA573	ABEA574	ABEA575	ABEA576	ABEA577	ABEA578	ABEA579	ABEA580	ABEA581	ABEA582	ABEA583	ABEA584	ABEA585	ABEA586	ABEA587	ABEA588	ABEA589	ABEA590	ABEA591	ABEA592	ABEA593	ABEA594	ABEA595	ABEA596	ABEA597	ABEA598	ABEA599	ABEA600	ABEA601	ABEA602	ABEA603	ABEA604	ABEA605	ABEA606	ABEA607	ABEA608	ABEA609	ABEA610	ABEA611	ABEA612	ABEA613	ABEA614	ABEA615	ABEA616	ABEA617	ABEA618	ABEA619	ABEA620	ABEA621	ABEA622	ABEA623	ABEA624	ABEA625	ABEA626	ABEA627	ABEA628	ABEA629	ABEA630	ABEA631	ABEA632	ABEA633	ABEA634	ABEA635	ABEA636	ABEA637	ABEA638	ABEA639	ABEA640	ABEA641	ABEA642	ABEA643	ABEA644	ABEA645	ABEA646	ABEA647	ABEA648	ABEA649	ABEA650	ABEA651	ABEA652	ABEA653	ABEA654	ABEA655	ABEA656	ABEA657	ABEA658	ABEA659	ABEA660	ABEA661	ABEA662	ABEA663	ABEA664	ABEA665	ABEA666	ABEA667	ABEA668	ABEA669	ABEA670	ABEA671	ABEA672	ABEA673	ABEA674	ABEA675	ABEA676	ABEA677	ABEA678	ABEA679	ABEA680	ABEA681	ABEA682	ABEA683	ABEA684	ABEA685	ABEA686	ABEA687	ABEA688	ABEA689	ABEA690	ABEA691	ABEA692	ABEA693	ABEA694	ABEA695	ABEA696	ABEA697	ABEA698	ABEA699	ABEA700	ABEA701	ABEA702	ABEA703	ABEA704	ABEA705	ABEA706	ABEA707	ABEA708	ABEA709	ABEA710	ABEA711	ABEA712	ABEA713	ABEA714	ABEA715	ABEA716	ABEA717	ABEA718	ABEA719	ABEA720	ABEA721	ABEA722	ABEA723	ABEA724	ABEA725	ABEA726	ABEA727	ABEA728	ABEA729	ABEA730	ABEA731	ABEA732	ABEA733	ABEA734	ABEA735	ABEA736	ABEA737	ABEA738	ABEA739	ABEA740	ABEA741	ABEA742	ABEA743	ABEA744	ABEA745	ABEA746	ABEA747	ABEA748	ABEA749	ABEA750	ABEA751	ABEA752	ABEA753	ABEA754	ABEA755	ABEA756	ABEA757	ABEA758	ABEA759	ABEA760	ABEA761	ABEA762	ABEA763	ABEA764	ABEA765	ABEA766	ABEA767	ABEA768	ABEA769	ABEA770	ABEA771	ABEA772	ABEA773	ABEA774	ABEA775	ABEA776	ABEA777	ABEA778	ABEA779	ABEA780	ABEA781	ABEA782	ABEA783	ABEA784	ABEA785	ABEA786	ABEA787	ABEA788	ABEA789	ABEA790	ABEA791	ABEA792	ABEA793	ABEA794	ABEA795	ABEA796	ABEA797	ABEA798	ABEA799	ABEA800	ABEA801	ABEA802	ABEA803	ABEA804	ABEA805	ABEA806	ABEA807	ABEA808	ABEA809	ABEA810	ABEA811	ABEA812	ABEA813	ABEA814	ABEA815	ABEA816	ABEA817	ABEA818	ABEA819	ABEA820	ABEA821	ABEA822	ABEA823	ABEA824	ABEA825	ABEA826	ABEA827	ABEA828	ABEA829	ABEA830	ABEA831	ABEA832	ABEA833	ABEA834	ABEA835	ABEA836	ABEA837	ABEA838	ABEA839	ABEA840	ABEA841	ABEA842	ABEA843	ABEA844	ABEA845	ABEA846	ABEA847	ABEA848	ABEA849	ABEA850	ABEA851	ABEA852	ABEA853	ABEA854	ABEA855	ABEA856	ABEA857	ABEA858	ABEA859	ABEA860	ABEA861	ABEA862	ABEA863	ABEA864	ABEA865	ABEA866	ABEA867	ABEA868	ABEA869	ABEA870	ABEA871	ABEA872	ABEA873	ABEA874	ABEA875	ABEA876	ABEA877	ABEA878	ABEA879	ABEA880	ABEA881	ABEA882	ABEA883	ABEA884	ABEA885	ABEA886	ABEA887	ABEA888	ABEA889	ABEA890	ABEA891	ABEA892	ABEA893	ABEA894	ABEA895	ABEA896	ABEA897	ABEA898	ABEA899	ABEA900	ABEA901	ABEA902	ABEA903	ABEA904	ABEA905	ABEA906	ABEA907	ABEA908	ABEA909	ABEA910	ABEA911	ABEA912	ABEA913	ABEA914	ABEA915	ABEA916	ABEA917	ABEA918	ABEA919	ABEA920	ABEA921	ABEA922	ABEA923	ABEA924	ABEA925	ABEA926	ABEA927	ABEA928	ABEA929	ABEA930	ABEA931	ABEA932	ABEA933	ABEA934	ABEA935	ABEA936	ABEA937	ABEA938	ABEA939	ABEA940	ABEA941	ABEA942	ABEA943	ABEA944	ABEA945	ABEA946	ABEA947	ABEA948	ABEA949	ABEA950	ABEA951	ABEA952	ABEA953	ABEA954	ABEA955	ABEA956	ABEA957	ABEA958	ABEA959	ABEA960	ABEA961	ABEA962	ABEA963	ABEA964	ABEA965	ABEA966	ABEA967	ABEA968	ABEA969	ABEA970	ABEA971	ABEA972	ABEA973	ABEA974	ABEA975	ABEA976	ABEA977	ABEA978	ABEA979	ABEA980	ABEA981	ABEA982	ABEA983	ABEA984	ABEA985	ABEA986	ABEA987	ABEA988	ABEA989	ABEA990	ABEA991	ABEA992	ABEA993	ABEA994	ABEA995	ABEA996	ABEA997	ABEA998	ABEA999	ABEA1000
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[illegible]



54



PCGENE	ALLANOTIS	ALL Virens (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PROTEIN	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	341-375						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	341-378						
ENV POLYPROTEIN	ENV POLYPROTEIN	AVIAN RETICULOENDOTHELITIS VIRUS	420-422						
ENV POLYPROTEIN	ENV POLYPROTEIN	AVIAN SPLEEN NECROSIS VIRUS	420-428						
ENV POLYPROTEIN	ENV POLYPROTEIN	BABOON ENDOGENOUS VIRUS (STRAIN MT)	100-416						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE DAUNODENEFICIENCY VIRUS (ISOLATE 106)	10-44	10-122	221-235	530-610	635-691		
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE DAUNODENEFICIENCY VIRUS (ISOLATE 117)	10-44	10-122	139-193	530-584	559-639	664-724	
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (AMERICAN ISOLATE FLK)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (AUSTRALIAN ISOLATE)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (AMERICAN ISOLATE VDM)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (BELGIAN ISOLATE LR215)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (BELGIAN ISOLATE LB19)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	BOVINE LEUKAEMIA VIRUS (JAPANESE ISOLATE BLV-1)	104-379						
ENV POLYPROTEIN	ENV POLYPROTEIN	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	137-196						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN GA)	134-193	615-726	711-781	843-905			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-1)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-2)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-3)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-4)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-5)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-6)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-7)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-8)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-9)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-10)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-11)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-12)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-13)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-14)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-15)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-16)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-17)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-18)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-19)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-20)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-21)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-22)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-23)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-24)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-25)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-26)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-27)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-28)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-29)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-30)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-31)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-32)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-33)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-34)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-35)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-36)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-37)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-38)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-39)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-40)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-41)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-42)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-43)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-44)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-45)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-46)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-47)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-48)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-49)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-50)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-51)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-52)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-53)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-54)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-55)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-56)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-57)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-58)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-59)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-60)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-61)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-62)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-63)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-64)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-65)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-66)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-67)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-68)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-69)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-70)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-71)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-72)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-73)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-74)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-75)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-76)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-77)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-78)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-79)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-80)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-81)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-82)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-83)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-84)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-85)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-86)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-87)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-88)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-89)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-90)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-91)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-92)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-93)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-94)	18-76	436-535	535-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3							



56



PCGENE	ALLIOTHS	ALL Virus (no better description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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[illegible]



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[illegible]



FIGURE	ALL NOTES	ALL VIRUSES (as bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FIGURE 1	PROTEIN	HUMAN ADENOVIRUS TYPE 12	48-137							
FIGURE 2	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 41	67-126							
FIGURE 3	HEXON-ASSOCIATED PROTEIN	CANINE ADENOVIRUS TYPE 1	53-103							
FIGURE 4	HEXON-ASSOCIATED PROTEIN	TUPAIA ADENOVIRUS	61-109							
FIGURE 5	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	341-386	131-467	151-424					
FIGURE 6	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 5	320-379							
FIGURE 7	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 40	301-332	601-649	551-587					
FIGURE 8	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 40	306-333	551-589						
FIGURE 9	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 41	301-344	551-589	546-578	701-739				
FIGURE 10	HEXON-ASSOCIATED PROTEIN	BOVINE ADENOVIRUS TYPE 1	310-393	453-489						
FIGURE 11	HEXON-ASSOCIATED PROTEIN	COMPOX VIRUS	110-131							
FIGURE 12	HEXON-ASSOCIATED PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA11V)	1-44	378-419						
FIGURE 13	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DA)	378-420							
FIGURE 14	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DARI 1)	5-37	378-419						
FIGURE 15	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CHI-1841)	5-37	378-419						
FIGURE 16	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DDI)	5-37	378-419						
FIGURE 17	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DDI)	5-37	378-419						
FIGURE 18	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN S-IAPAN)	5-37	378-419						
FIGURE 19	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV147)	5-37	378-419						
FIGURE 20	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	5-37	378-419						
FIGURE 21	HEXON-ASSOCIATED PROTEIN	CARNATION ETCHED RING VIRUS	1-31	372-406						
FIGURE 22	HEXON-ASSOCIATED PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN D53)	1-48	372-419	496-532					
FIGURE 23	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	53-98	290-324						
FIGURE 24	HEXON-ASSOCIATED PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	311-365							
FIGURE 25	HEXON-ASSOCIATED PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN ANGELOTTI)	311-365							
FIGURE 26	HEXON-ASSOCIATED PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	324-362							
FIGURE 27	HEXON-ASSOCIATED PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	406-500							
FIGURE 28	HEXON-ASSOCIATED PROTEIN	BOVINE HERPESVIRUS TYPE 1 (ISOLATE HV535A)	341-375							
FIGURE 29	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	51-99	361-395						
FIGURE 30	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN SMITH)	60-112	290-340	647-691					
FIGURE 31	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	399-331	101-137						
FIGURE 32	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	190-224							
FIGURE 33	HEXON-ASSOCIATED PROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN K23)	102-106							
FIGURE 34	HEXON-ASSOCIATED PROTEIN	MAKKE'S DISEASE HERPESVIRUS (STRAIN GA)	920-934							
FIGURE 35	HEXON-ASSOCIATED PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	307-341							
FIGURE 36	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	241-275							
FIGURE 37	HEXON-ASSOCIATED PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	213-216							
FIGURE 38	HEXON-ASSOCIATED PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	191-239	218-308						
FIGURE 39	HEXON-ASSOCIATED PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	97-121							
FIGURE 40	HEXON-ASSOCIATED PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	99-133							
FIGURE 41	HEXON-ASSOCIATED PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	48-53							
FIGURE 42	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	13-43							
FIGURE 43	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-102							
FIGURE 44	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	280-314							
FIGURE 45	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 46	HEXON-ASSOCIATED PROTEIN	ABELSON MURINE LEUKEMIA VIRUS	172-227	283-304						
FIGURE 47	HEXON-ASSOCIATED PROTEIN	ACT1 MURINE LEUKEMIA VIRUS	21-44	104-178						
FIGURE 48	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 49	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 50	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 51	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 52	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 53	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 54	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 55	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 56	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 57	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 58	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 59	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 60	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 61	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 62	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 63	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 64	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 65	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 66	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 67	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 68	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 69	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 70	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 71	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 72	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 73	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 74	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 75	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 76	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 77	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 78	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 79	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 80	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 81	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 82	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 83	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 84	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 85	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 86	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 87	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 88	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 89	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 90	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 91	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 92	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 93	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 94	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 95	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 96	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 97	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 98	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 99	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							
FIGURE 100	HEXON-ASSOCIATED PROTEIN	HERPESVIRUS SAIRURI (STRAIN 11)	213-231							



[illegible]



[illegible]



PCGENE	ALLNOTES	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8	ABCA9	ABCA10	ABCA11	ABCA12	ABCA13	ABCA14	ABCA15	ABCA16	ABCA17	ABCA18	ABCA19	ABCA20	ABCA21	ABCA22	ABCA23	ABCA24	ABCA25	ABCA26	ABCA27	ABCA28	ABCA29	ABCA30	ABCA31	ABCA32	ABCA33	ABCA34	ABCA35	ABCA36	ABCA37	ABCA38	ABCA39	ABCA40	ABCA41	ABCA42	ABCA43	ABCA44	ABCA45	ABCA46	ABCA47	ABCA48	ABCA49	ABCA50	ABCA51	ABCA52	ABCA53	ABCA54	ABCA55	ABCA56	ABCA57	ABCA58	ABCA59	ABCA60	ABCA61	ABCA62	ABCA63	ABCA64	ABCA65	ABCA66	ABCA67	ABCA68	ABCA69	ABCA70	ABCA71	ABCA72	ABCA73	ABCA74	ABCA75	ABCA76	ABCA77	ABCA78	ABCA79	ABCA80	ABCA81	ABCA82	ABCA83	ABCA84	ABCA85	ABCA86	ABCA87	ABCA88	ABCA89	ABCA90	ABCA91	ABCA92	ABCA93	ABCA94	ABCA95	ABCA96	ABCA97	ABCA98	ABCA99	ABCA100	ABCA101	ABCA102	ABCA103	ABCA104	ABCA105	ABCA106	ABCA107	ABCA108	ABCA109	ABCA110	ABCA111	ABCA112	ABCA113	ABCA114	ABCA115	ABCA116	ABCA117	ABCA118	ABCA119	ABCA120	ABCA121	ABCA122	ABCA123	ABCA124	ABCA125	ABCA126	ABCA127	ABCA128	ABCA129	ABCA130	ABCA131	ABCA132	ABCA133	ABCA134	ABCA135	ABCA136	ABCA137	ABCA138	ABCA139	ABCA140	ABCA141	ABCA142	ABCA143	ABCA144	ABCA145	ABCA146	ABCA147	ABCA148	ABCA149	ABCA150	ABCA151	ABCA152	ABCA153	ABCA154	ABCA155	ABCA156	ABCA157	ABCA158	ABCA159	ABCA160	ABCA161	ABCA162	ABCA163	ABCA164	ABCA165	ABCA166	ABCA167	ABCA168	ABCA169	ABCA170	ABCA171	ABCA172	ABCA173	ABCA174	ABCA175	ABCA176	ABCA177	ABCA178	ABCA179	ABCA180	ABCA181	ABCA182	ABCA183	ABCA184	ABCA185	ABCA186	ABCA187	ABCA188	ABCA189	ABCA190	ABCA191	ABCA192	ABCA193	ABCA194	ABCA195	ABCA196	ABCA197	ABCA198	ABCA199	ABCA200	ABCA201	ABCA202	ABCA203	ABCA204	ABCA205	ABCA206	ABCA207	ABCA208	ABCA209	ABCA210	ABCA211	ABCA212	ABCA213	ABCA214	ABCA215	ABCA216	ABCA217	ABCA218	ABCA219	ABCA220	ABCA221	ABCA222	ABCA223	ABCA224	ABCA225	ABCA226	ABCA227	ABCA228	ABCA229	ABCA230	ABCA231	ABCA232	ABCA233	ABCA234	ABCA235	ABCA236	ABCA237	ABCA238	ABCA239	ABCA240	ABCA241	ABCA242	ABCA243	ABCA244	ABCA245	ABCA246	ABCA247	ABCA248	ABCA249	ABCA250	ABCA251	ABCA252	ABCA253	ABCA254	ABCA255	ABCA256	ABCA257	ABCA258	ABCA259	ABCA260	ABCA261	ABCA262	ABCA263	ABCA264	ABCA265	ABCA266	ABCA267	ABCA268	ABCA269	ABCA270	ABCA271	ABCA272	ABCA273	ABCA274	ABCA275	ABCA276	ABCA277	ABCA278	ABCA279	ABCA280	ABCA281	ABCA282	ABCA283	ABCA284	ABCA285	ABCA286	ABCA287	ABCA288	ABCA289	ABCA290	ABCA291	ABCA292	ABCA293	ABCA294	ABCA295	ABCA296	ABCA297	ABCA298	ABCA299	ABCA300	ABCA301	ABCA302	ABCA303	ABCA304	ABCA305	ABCA306	ABCA307	ABCA308	ABCA309	ABCA310	ABCA311	ABCA312	ABCA313	ABCA314	ABCA315	ABCA316	ABCA317	ABCA318	ABCA319	ABCA320	ABCA321	ABCA322	ABCA323	ABCA324	ABCA325	ABCA326	ABCA327	ABCA328	ABCA329	ABCA330	ABCA331	ABCA332	ABCA333	ABCA334	ABCA335	ABCA336	ABCA337	ABCA338	ABCA339	ABCA340	ABCA341	ABCA342	ABCA343	ABCA344	ABCA345	ABCA346	ABCA347	ABCA348	ABCA349	ABCA350	ABCA351	ABCA352	ABCA353	ABCA354	ABCA355	ABCA356	ABCA357	ABCA358	ABCA359	ABCA360	ABCA361	ABCA362	ABCA363	ABCA364	ABCA365	ABCA366	ABCA367	ABCA368	ABCA369	ABCA370	ABCA371	ABCA372	ABCA373	ABCA374	ABCA375	ABCA376	ABCA377	ABCA378	ABCA379	ABCA380	ABCA381	ABCA382	ABCA383	ABCA384	ABCA385	ABCA386	ABCA387	ABCA388	ABCA389	ABCA390	ABCA391	ABCA392	ABCA393	ABCA394	ABCA395	ABCA396	ABCA397	ABCA398	ABCA399	ABCA400	ABCA401	ABCA402	ABCA403	ABCA404	ABCA405	ABCA406	ABCA407	ABCA408	ABCA409	ABCA410	ABCA411	ABCA412	ABCA413	ABCA414	ABCA415	ABCA416	ABCA417	ABCA418	ABCA419	ABCA420	ABCA421	ABCA422	ABCA423	ABCA424	ABCA425	ABCA426	ABCA427	ABCA428	ABCA429	ABCA430	ABCA431	ABCA432	ABCA433	ABCA434	ABCA435	ABCA436	ABCA437	ABCA438	ABCA439	ABCA440	ABCA441	ABCA442	ABCA443	ABCA444	ABCA445	ABCA446	ABCA447	ABCA448	ABCA449	ABCA450	ABCA451	ABCA452	ABCA453	ABCA454	ABCA455	ABCA456	ABCA457	ABCA458	ABCA459	ABCA460	ABCA461	ABCA462	ABCA463	ABCA464	ABCA465	ABCA466	ABCA467	ABCA468	ABCA469	ABCA470	ABCA471	ABCA472	ABCA473	ABCA474	ABCA475	ABCA476	ABCA477	ABCA478	ABCA479	ABCA480	ABCA481	ABCA482	ABCA483	ABCA484	ABCA485	ABCA486	ABCA487	ABCA488	ABCA489	ABCA490	ABCA491	ABCA492	ABCA493	ABCA494	ABCA495	ABCA496	ABCA497	ABCA498	ABCA499	ABCA500	ABCA501	ABCA502	ABCA503	ABCA504	ABCA505	ABCA506	ABCA507	ABCA508	ABCA509	ABCA510	ABCA511	ABCA512	ABCA513	ABCA514	ABCA515	ABCA516	ABCA517	ABCA518	ABCA519	ABCA520	ABCA521	ABCA522	ABCA523	ABCA524	ABCA525	ABCA526	ABCA527	ABCA528	ABCA529	ABCA530	ABCA531	ABCA532	ABCA533	ABCA534	ABCA535	ABCA536	ABCA537	ABCA538	ABCA539	ABCA540	ABCA541	ABCA542	ABCA543	ABCA544	ABCA545	ABCA546	ABCA547	ABCA548	ABCA549	ABCA550	ABCA551	ABCA552	ABCA553	ABCA554	ABCA555	ABCA556	ABCA557	ABCA558	ABCA559	ABCA560	ABCA561	ABCA562	ABCA563	ABCA564	ABCA565	ABCA566	ABCA567	ABCA568	ABCA569	ABCA570	ABCA571	ABCA572	ABCA573	ABCA574	ABCA575	ABCA576	ABCA577	ABCA578	ABCA579	ABCA580	ABCA581	ABCA582	ABCA583	ABCA584	ABCA585	ABCA586	ABCA587	ABCA588	ABCA589	ABCA590	ABCA591	ABCA592	ABCA593	ABCA594	ABCA595	ABCA596	ABCA597	ABCA598	ABCA599	ABCA600	ABCA601	ABCA602	ABCA603	ABCA604	ABCA605	ABCA606	ABCA607	ABCA608	ABCA609	ABCA610	ABCA611	ABCA612	ABCA613	ABCA614	ABCA615	ABCA616	ABCA617	ABCA618	ABCA619	ABCA620	ABCA621	ABCA622	ABCA623	ABCA624	ABCA625	ABCA626	ABCA627	ABCA628	ABCA629	ABCA630	ABCA631	ABCA632	ABCA633	ABCA634	ABCA635	ABCA636	ABCA637	ABCA638	ABCA639	ABCA640	ABCA641	ABCA642	ABCA643	ABCA644	ABCA645	ABCA646	ABCA647	ABCA648	ABCA649	ABCA650	ABCA651	ABCA652	ABCA653	ABCA654	ABCA655	ABCA656	ABCA657	ABCA658	ABCA659	ABCA660	ABCA661	ABCA662	ABCA663	ABCA664	ABCA665	ABCA666	ABCA667	ABCA668	ABCA669	ABCA670	ABCA671	ABCA672	ABCA673	ABCA674	ABCA675	ABCA676	ABCA677	ABCA678	ABCA679	ABCA680	ABCA681	ABCA682	ABCA683	ABCA684	ABCA685	ABCA686	ABCA687	ABCA688	ABCA689	ABCA690	ABCA691	ABCA692	ABCA693	ABCA694	ABCA695	ABCA696	ABCA697	ABCA698	ABCA699	ABCA700	ABCA701	ABCA702	ABCA703	ABCA704	ABCA705	ABCA706	ABCA707	ABCA708	ABCA709	ABCA710	ABCA711	ABCA712	ABCA713	ABCA714	ABCA715	ABCA716	ABCA717	ABCA718	ABCA719	ABCA720	ABCA721	ABCA722	ABCA723	ABCA724	ABCA725	ABCA726	ABCA727	ABCA728	ABCA729	ABCA730	ABCA731	ABCA732	ABCA733	ABCA734	ABCA735	ABCA736	ABCA737	ABCA738	ABCA739	ABCA740	ABCA741	ABCA742	ABCA743	ABCA744	ABCA745	ABCA746	ABCA747	ABCA748	ABCA749	ABCA750	ABCA751	ABCA752	ABCA753	ABCA754	ABCA755	ABCA756	ABCA757	ABCA758	ABCA759	ABCA760	ABCA761	ABCA762	ABCA763	ABCA764	ABCA765	ABCA766	ABCA767	ABCA768	ABCA769	ABCA770	ABCA771	ABCA772	ABCA773	ABCA774	ABCA775	ABCA776	ABCA777	ABCA778	ABCA779	ABCA780	ABCA781	ABCA782	ABCA783	ABCA784	ABCA785	ABCA786	ABCA787	ABCA788	ABCA789	ABCA790	ABCA791	ABCA792	ABCA793	ABCA794	ABCA795	ABCA796	ABCA797	ABCA798	ABCA799	ABCA800	ABCA801	ABCA802	ABCA803	ABCA804	ABCA805	ABCA806	ABCA807	ABCA808	ABCA809	ABCA810	ABCA811	ABCA812	ABCA813	ABCA814	ABCA815	ABCA816	ABCA817	ABCA818	ABCA819	ABCA820	ABCA821	ABCA822	ABCA823	ABCA824	ABCA825	ABCA826	ABCA827	ABCA828	ABCA829	ABCA830	ABCA831	ABCA832	ABCA833	ABCA834	ABCA835	ABCA836	ABCA837	ABCA838	ABCA839	ABCA840	ABCA841	ABCA842	ABCA843	ABCA844	ABCA845	ABCA846	ABCA847	ABCA848	ABCA849	ABCA850	ABCA851	ABCA852	ABCA853	ABCA854	ABCA855	ABCA856	ABCA857	ABCA858	ABCA859	ABCA860	ABCA861	ABCA862	ABCA863	ABCA864	ABCA865	ABCA866	ABCA867	ABCA868	ABCA869	ABCA870	ABCA871	ABCA872	ABCA873	ABCA874	ABCA875	ABCA876	ABCA877	ABCA878	ABCA879	ABCA880	ABCA881	ABCA882	ABCA883	ABCA884	ABCA885	ABCA886	ABCA887	ABCA888	ABCA889	ABCA890	ABCA891	ABCA892	ABCA893	ABCA894	ABCA895	ABCA896	ABCA897	ABCA898	ABCA899	ABCA900	ABCA901	ABCA902	ABCA903	ABCA904	ABCA905	ABCA906	ABCA907	ABCA908	ABCA909	ABCA910	ABCA911	ABCA912	ABCA913	ABCA914	ABCA915	ABCA916	ABCA917	ABCA918	ABCA919	ABCA920	ABCA921	ABCA922	ABCA923	ABCA924	ABCA925	ABCA926	ABCA927	ABCA928	ABCA929	ABCA930	ABCA931	ABCA932	ABCA933	ABCA934	ABCA935	ABCA936	ABCA937	ABCA938	ABCA939	ABCA940	ABCA941	ABCA942	ABCA943	ABCA944	ABCA945	ABCA946	ABCA947	ABCA948	ABCA949	ABCA950	ABCA951	ABCA952	ABCA953	ABCA954	ABCA955	ABCA956	ABCA957	ABCA958	ABCA959	ABCA960	ABCA961	ABCA962	ABCA963	ABCA964	ABCA965	ABCA966	ABCA967	ABCA968	ABCA969	ABCA970	ABCA971	ABCA972	ABCA973	ABCA974	ABCA975	ABCA976	ABCA977	ABCA978	ABCA979	ABCA980	ABCA981	ABCA982	ABCA983	ABCA984	ABCA985	ABCA986	ABCA987	ABCA988	ABCA989	ABCA990	ABCA991	ABCA992	ABCA993	ABCA994	ABCA995	ABCA996	ABCA997	ABCA998	ABCA999	ABCA1000
PCGENE	ALLNOTES	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8	ABCA9	ABCA10	ABCA11	ABCA12	ABCA13	ABCA14	ABCA15	ABCA16	ABCA17	ABCA18	ABCA19	ABCA20	ABCA21	ABCA22	ABCA23	ABCA24	ABCA25	ABCA26	ABCA27	ABCA28	ABCA29	ABCA30	ABCA31	ABCA32	ABCA33	ABCA34	ABCA35	ABCA36	ABCA37	ABCA38	ABCA39	ABCA40	ABCA41	ABCA42	ABCA43	ABCA44	ABCA45	ABCA46	ABCA47	ABCA48	ABCA49	ABCA50	ABCA51	ABCA52	ABCA53	ABCA54	ABCA55	ABCA56	ABCA57	ABCA58	ABCA59	ABCA60	ABCA61	ABCA62	ABCA63	ABCA64	ABCA65	ABCA66	ABCA67	ABCA68	ABCA69	ABCA70	ABCA71	ABCA72	ABCA73	ABCA74	ABCA75	ABCA76	ABCA77	ABCA78	ABCA79	ABCA80	ABCA81	ABCA82	ABCA83	ABCA84	ABCA85	ABCA86	ABCA87	ABCA88	ABCA89	ABCA90	ABCA91	ABCA92	ABCA93	ABCA94	ABCA95	ABCA96	ABCA97	ABCA98	ABCA99	ABCA100	ABCA101	ABCA102	ABCA103	ABCA104	ABCA105	ABCA106	ABCA107	ABCA108	ABCA109	ABCA110	ABCA111	ABCA112	ABCA113	ABCA114	ABCA115	ABCA116	ABCA117	ABCA118	ABCA119	ABCA120	ABCA121	ABCA122	ABCA123	ABCA124	ABCA125	ABCA126	ABCA127	ABCA128	ABCA129	ABCA130	ABCA131	ABCA132	ABCA133	ABCA134	ABCA135	ABCA136	ABCA137	ABCA138	ABCA139	ABCA140	ABCA141	ABCA142	ABCA143	ABCA144	ABCA145	ABCA146	ABCA147	ABCA148	ABCA149	ABCA150	ABCA151	ABCA152	ABCA153	ABCA154	ABCA155	ABCA156	ABCA157	ABCA158	ABCA159	ABCA160	ABCA161	ABCA162	ABCA163	ABCA164	ABCA165	ABCA166	ABCA167	ABCA168	ABCA169	ABCA170	ABCA171	ABCA172	ABCA173	ABCA174	ABCA175	ABCA176	ABCA177	ABCA178	ABCA179	ABCA180	ABCA181	ABCA182	ABCA183	ABCA184	ABCA185	ABCA186	ABCA187	ABCA188	ABCA189	ABCA190	ABCA191	ABCA192	ABCA193	ABCA194	ABCA195	ABCA196	ABCA197	ABCA198	ABCA199	ABCA200	ABCA201	ABCA202	ABCA203	ABCA204	ABCA205	ABCA206	ABCA207	ABCA208	ABCA209	ABCA210	ABCA211	ABCA212	ABCA213	ABCA214	ABCA215	ABCA216	ABCA217	ABCA218	ABCA219	ABCA220	ABCA221	ABCA222	ABCA223	ABCA224	ABCA225	ABCA226	ABCA227	ABCA228	ABCA229	ABCA230	ABCA231	ABCA232	ABCA233	ABCA234	ABCA235	ABCA236	ABCA237	ABCA238	ABCA239	ABCA240	ABCA241	ABCA242	ABCA243	ABCA244	ABCA245	ABCA246	ABCA247	ABCA248	ABCA249	ABCA250	ABCA251	ABCA252	ABCA253	ABCA254	ABCA255	ABCA256																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								



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ACCIONE	ALLMOTIS	ALL VITRUS (no better description)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PPOL1 BATJAU	GENOME POLYPROTEIN 2	BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1)	649-732	739-772						
PPOL1 GFLV	GENOME POLYPROTEIN	GRAPEVINE FANLEAF VIRUS	361-406	341-402						
PPOL1 TRAVS	RNA3 POLYPROTEIN		6-18							
PPOL1 TRAVR	RNA3 POLYPROTEIN	TOMATO BLACK RING VIRUS (STRAIN S)	131-206	131-168						
PPOL1 BOVEV	GENOME POLYPROTEIN	TOMATO RINGSPOT VIRUS (ISOLATE RA SPRIERAY)	949-886	1008-1064	1332-1416	1418-1507	1574-1617			
PPOL1 BVDVN	GENOME POLYPROTEIN	BOVINE ENTEROVIRUS (STRAIN VG-1-27)	344-339	444-491	429-463	1023-1074	1201-1244	1392-1443	1869-1910	2126-2160
PPOL1 BVDVS	GENOME POLYPROTEIN	BOVINE VIRAL DIARRHEA VIRUS (ISOLATE MADL)	243-239	444-491	429-463	1023-1074	1201-1244	1392-1443	1778-1820	2118-2170
PPOL1 BYMV	GENOME POLYPROTEIN	BEAN YELLOW MOSAIC VIRUS (STRAIN SD-1)	96-130							
PPOL1 COXA2	GENOME POLYPROTEIN	COXSACKIEVIRUS A21 (STRAIN COE)	6-43	163-194	164-208	1045-1100	1408-1546	1607-1648	1803-1839	1901-1946
PPOL1 COXA3	GENOME POLYPROTEIN	COXSACKIEVIRUS A9 (STRAIN GRUGGS)	13-49	1040-1086	1092-1140					
PPOL1 COXA9	GENOME POLYPROTEIN	COXSACKIEVIRUS B1	13-49	1031-1067	1076-1121					
PPOL1 COXB1	GENOME POLYPROTEIN	COXSACKIEVIRUS B1	13-49	1034-1070	1076-1121					
PPOL1 COXB3	GENOME POLYPROTEIN	COXSACKIEVIRUS B4	13-49	642-681	1022-1068	1073-1123				
PPOL1 COXB4	GENOME POLYPROTEIN	COXSACKIEVIRUS B3	13-49	1024-1070	1076-1121					
PPOL1 COXB5	GENOME POLYPROTEIN		120-134							
PPOL1 CYVV	GENOME POLYPROTEIN	CLOVER YELLOW VEIN VIRUS	74-108							
PPOL1 DEN18	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN B16-1)	74-108							
PPOL1 DEN19	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN A1F 31-40)	74-108							
PPOL1 DEN20	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN CV163677)	74-108	832-873	960-994	1142-1179	1386-1420	1614-1648	2318-2354	2946-3016
PPOL1 DEN21	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE 327990)	74-108	832-873	961-995	1143-1180				
PPOL1 DEN22	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN WESTERN PACIFIC)	74-108	832-873	961-995	1143-1180				
PPOL1 DEN23	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA M1)	448-492							
PPOL1 DEN24	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA M2)	448-492							
PPOL1 DEN25	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 16481)	74-108	728-777	961-995	1146-1180	1246-1280	1418-1452	1615-1649	2317-2351
PPOL1 DEN26	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 16481-PK53)	74-108	728-777	961-995	1146-1180	1246-1280	1418-1452	1615-1649	2481-2531
PPOL1 DEN27	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN D2-64)	728-777							
PPOL1 DEN28	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN TH-26)	497-546							
PPOL1 DEN29	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN JAMAICA)	74-108	728-777	961-995	1146-1180	1246-1280	1418-1452	1615-1649	2317-2351
PPOL1 DEN30	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN NEW GUINEA C)	312-247	198-432						
PPOL1 DEN31	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PR19951)	74-108	728-777	832-873	961-995	1146-1180	1246-1280	1418-1452	1615-1649
PPOL1 DEN32	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN TONGA 1974)	448-497	532-595	641-715	846-900	946-1000	1205-1239		
PPOL1 DEN33	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PUO-211)	414-463							
PPOL1 DEN34	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3	810-873	919-993	1384-1419	2234-2318	2480-2521	2704-2718	2940-2978	2980-3014
PPOL1 DEN35	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4	951-993	1380-1414	2316-2353	2701-2733	2941-2973	3077-3011		
PPOL1 EN11G	GENOME POLYPROTEIN	ECHO VIRUS 11 (STRAIN GREGORY)	312-259	1078-1113						
PPOL1 EN12G	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS	1074-1115	1472-1518	1522-1570	1643-1706	1789-1833			
PPOL1 EN13G	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-B NONDIABETO)	143-179	1016-1117	1474-1520	1524-1572	1647-1708			
PPOL1 EN14G	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-D DIABETOGEN)	143-179	1016-1117	1474-1520	1524-1572	1647-1708			
PPOL1 EN15G	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN 37A)	143-179							
PPOL1 EN16G	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	78-112							
PPOL1 EN17G	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS (STRAIN A10-41)	221-255	394-428	578-612	1103-1153	1493-1528	2165-2200		
PPOL1 EN18G	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	220-254	391-427	577-611	1103-1164	1493-1528	2164-2199		
PPOL1 EN19G	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIBF5)	221-255	1103-1153	1493-1528	2164-2199				
PPOL1 EN20G	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1-SANTA PAU IC-5)	87-128	693-728						
PPOL1 EN21G	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1)	221-255	203-317	577-611					
PPOL1 EN22G	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE 1)	164-198							
PPOL1 EN23G	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN ALFORT)	440-493	616-660	695-729	1031-1070	1190-1225	1307-1343	1779-1820	2116-2170
PPOL1 EN24G	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESCIA)	2466-2500	2313-2359	2647-2703	3037-3098	3153-3199	3608-3640		
PPOL1 EN25G	GENOME POLYPROTEIN		440-493	616-660	695-729	1031-1070	1190-1225	1307-1343	1779-1820	2116-2170
PPOL1 EN26G	GENOME POLYPROTEIN		2466-2500	2313-2359	2647-2703	3037-3098	3153-3199	3608-3640	3616-3640	3618-3640
PPOL1 EN27G	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE BK)	1573-198	2318-2365						
PPOL1 EN28G	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE EC10)	61-99							



68







70



[illegible]



77



[illegible]



74



[illegible]



PCGENE	ALLNOTES	AB Virus: (no description)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	309-343	540-600	612-636	747-781	1064-1119	1216-1280	1499-1535	2000-2016
PRAPL SCOUR	RNA POLYMERASE BETA SUBUNIT	SEMOAI VIRUS (STRAIN 2)	2146-2216							
PRAPL SVSVR	RNA-DIRECTED RNA POLYMERASE	SEOL VIRUS (STRAIN 80-37)	98-139	174-208	557-591	635-686	731-765	1742-1776	1947-1981	1993-2027
PRAPL SYNY	RNA POLYMERASE BETA SUBUNIT	SOMAN VIRUS 3 (STRAIN 11004-WR)	547-637	747-781	1223-1280	1316-1353	1592-1626	1676-1715	2024-2058	
PRAPL TSWSB	RNA POLYMERASE BETA SUBUNIT	SOMCHUS YELLOW MEI VIRUS	760-794	821-859	977-1014	1089-1127	1179-1217	2058-2107		
PRAPL UUR	RNA-DIRECTED RNA POLYMERASE	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPNRI/BR)	44-101	199-433	518-573	589-634	1119-1153	1194-1238	1321-1379	1510-1572
			1484-1723	1837-1896	2073-2127	2156-2200	2206-2247	2312-2348	2376-2419	2806-2843
			127-187	281-321	616-674	1010-1071	1481-1515	2013-2049	2661-2698	
PRAPL VSVIN	RNA POLYMERASE	LUKUNDEMI VIRUS	115-158	674-715	720-763	1222-1267	1802-1836			
PRAPL VSVIO	RNA POLYMERASE BETA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)	210-238	674-715	720-763	1002-1036				
PRAPL VSVI	RNA POLYMERASE BETA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)	674-715	720-763	1016-1074	1742-1799	2066-2107			
PRAPL AGLSV	RNA POLYMERASE BETA SUBUNIT	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	228-262	557-596	916-950	1235-1269				
PRAPL BWYV	RNA-DIRECTED RNA POLYMERASE	APPLE CHLOROTIC LEAF SPOT VIRUS	304-341							
PRAPL BYDVI	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BEE WESTERN YELLOW VIRUS (ISOLATE FL-1)	234-285							
PRAPL BYDVP	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE MA-V-P51)	234-285							
PRAPL BYDVR	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE PAV)	234-285							
PRAPL CARAV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE P-P-V)	91-121							
PRAPL COMVS	PROBABLE RNA-DIRECTED RNA POLYMERASE	CANNON MOTTLE VIRUS	7-41	187-428	446-480	726-767	1445-1479			
PRAPL BVDV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	CUCUMBER GREEN MOTTLE MOSAIC VIRUS (WATERMELON STR)	384-422	446-484	709-757	771-809				
PRAPL BDDA	PUTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 32/70)	144-185	266-307	501-535	750-802				
PRAPL BBNV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	147-181	266-307	501-535	750-802				
PRAPL BPNV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE IASPER)	167-181	346-407	501-535	753-802				
PRAPL BPNVS	PUTATIVE RNA-DIRECTED RNA POLYMERASE	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE SP)	167-181	346-407	501-535	753-802				
PRAPL LYCVA	PUTATIVE RNA-DIRECTED RNA POLYMERASE	LYMPHOCTIC CHORIOENCEPHALITIS VIRUS (STRAIN ARMSTRON)	101-346	805-846	926-960	1509-1543	2090-2124			
PRAPL LYCVW	RNA POLYMERASE	LYMPHOCTIC CHORIOENCEPHALITIS VIRUS (STRAIN WE)	101-345							
PRAPL MCNV	RNA POLYMERASE	MAIZE CHLOROTIC MOTTLE VIRUS	181-215	697-731						
PRAPL PEANY	PROBABLE RNA-DIRECTED RNA POLYMERASE	PEA ENATION MOSAIC VIRUS	321-358							
PRAPL PLXVI	RNA-DIRECTED RNA POLYMERASE	POTATO LEAFROLL VIRUS (STRAIN 1)	316-373	423-457						
PRAPL PLXV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	316-373	423-457						
PRAPL PPNVS	PUTATIVE RNA-DIRECTED RNA POLYMERASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	321-362	602-634	627-661					
PRAPL RDNV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	466-700							
PRAPL REODV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	REOVIRUS (TYPE 2 / STRAIN DEARMON)	310-361							
PRAPL REOVI	RNA-DIRECTED RNA POLYMERASE	REOVIRUS (TYPE 1 / STRAIN LANG)	310-344							
PRAPL ROTBV	RNA-DIRECTED RNA POLYMERASE	BOVINE ROTAVIRUS (STRAIN N7)	60-96	122-167	204-245	534-569	579-621	639-686	690-724	771-805
PRAPL ROTBU	RNA-DIRECTED RNA POLYMERASE SUBUNIT VP1	BOVINE ROTAVIRUS (STRAIN UK)	60-96	122-167	204-245	534-569	579-621	639-686	690-724	771-805
PRAPL ROTVC	RNA-DIRECTED RNA POLYMERASE SUBUNIT VP1	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	3-46	235-299	335-397	478-510	510-520	564-607		
PRAPL ROTVO	RNA-DIRECTED RNA POLYMERASE SUBUNIT VP1	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	62-96	132-187	236-277	581-611	636-686	690-724	771-805	
PRAPL ROTSI	RNA-DIRECTED RNA POLYMERASE SUBUNIT VP1	SOMAN 11 ROTAVIRUS (STRAIN SAI1)	60-96	132-187	236-277	581-611	636-686	690-724	771-805	
PRAPL SBVLA	PROBABLE RNA-DIRECTED RNA POLYMERASE	SOUTHERN BEAN MOSAIC VIRUS	628-663							
PRAPL SCVLA	RNA-DIRECTED RNA POLYMERASE	SACCHAROMYCES CEREVISIAE VIRUS L-A	100-124	147-191						
PRAPL TACY	RNA POLYMERASE	TACABE VIRUS	155-204	220-278	375-416	484-518	691-723	1020-1081	1285-1319	1991-2015
PRAPL THNAV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	TABACCO MILD GREEN MOSAIC VIRUS (NAV STRAIN UD)	401-449	612-658	765-818					
PRAPL THVKA	PUTATIVE RNA-DIRECTED RNA POLYMERASE	TABACCO MOSAIC VIRUS (MULGARE)	3-37	401-433	665-699					
PRAPL THVTO	PUTATIVE RNA-DIRECTED RNA POLYMERASE	TABACCO MOSAIC VIRUS (STRAIN KOREAN)	3-37	401-433	665-699					
PRAPL THVVO	PUTATIVE RNA-DIRECTED RNA POLYMERASE	TABACCO MOSAIC VIRUS (STRAIN TOMATOL)	3-37	401-433	665-699					



PCGENE	ALLNOTES	AB Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN										
PRPP_BSLVA	RNA-DIRECTED RNA POLYMERASE	TOBACCO NECROSIS VIRUS (STRAIN D)	102-144							
PRPP_CDOVO	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN ASI198)	99-158							
PRPP_HSLV	RNA POLYMERASE ALPHA SUBUNIT	CANINE DISTEMPER VIRUS (STRAIN ONDELSTEPOORT)	312-373							
PRPP_HSLV1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS	99-158							
PRPP_HSLV2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 99-158)	160-216							
PRPP_HSLV3	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	99-158							
PRPP_MEASE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN 99-158)	160-216							
PRPP_MEAST	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDMONTON)	315-374							
PRPP_MEAST1	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN P-3-CA)	460-495							
PRPP_MEAST2	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAMAGATA-1)	460-495							
PRPP_MEAST3	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN SBL-1)	315-374							
PRPP_MEAST4	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDESA)	140-183							
PRPP_MEAST5	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDESA)	214-276							
PRPP_MEAST6	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDESA)	214-276							
PRPP_MEAST7	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/21)	100-134							
PRPP_MEAST8	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CHS)	100-138							
PRPP_MEAST9	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C35)	60-114							
PRPP_MEAST10	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C39)	60-114							
PRPP_MEAST11	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-573)	60-114							
PRPP_MEAST12	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-4730)	60-114							
PRPP_MEAST13	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	218-281							
PRPP_MEAST14	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	218-281							
PRPP_MEAST15	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	311-320							
PRPP_MEAST16	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47845)	410-499							
PRPP_MEAST17	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	4-38							
PRPP_MEAST18	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 44-333)	222-285							
PRPP_MEAST19	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS	137-174							
PRPP_MEAST20	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN A'VOI)	93-127							
PRPP_MEAST21	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN CVS-11)	93-127							
PRPP_MEAST22	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN ERA), AND (STRAIN PM)	93-127							
PRPP_MEAST23	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN PV)	93-127							
PRPP_MEAST24	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN SAD B19)	93-127							
PRPP_MEAST25	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 694)	313-364							
PRPP_MEAST26	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN FUSION)	313-364							
PRPP_MEAST27	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN HARRIS)	313-364							
PRPP_MEAST28	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 2)	313-364							
PRPP_MEAST29	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS 5 (STRAIN W)	313-364							
PRPP_MEAST30	RNA POLYMERASE ALPHA SUBUNIT	SONCHUS YELLOW NET VIRUS	203-278							
PRPP_MEAST31	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C-43)	138-173							
PRPP_MEAST32	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN A-43)	138-173							
PRPP_MEAST33	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 5-37)	138-173							
PRPP_MEAST34	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	138-173							
PRPP_MEAST35	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	138-173							
PRPP_MEAST36	RNA POLYMERASE ALPHA SUBUNIT	AMEBIC MOOREI ENTOMOPHAGUS	233-264							
PRPP_MEAST37	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST38	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST39	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST40	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST41	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST42	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST43	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST44	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST45	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST46	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST47	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST48	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST49	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST50	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST51	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST52	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST53	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST54	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST55	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST56	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST57	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST58	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST59	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST60	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST61	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST62	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST63	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST64	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST65	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST66	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST67	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST68	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST69	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST70	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST71	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST72	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST73	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST74	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST75	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST76	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST77	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST78	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST79	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST80	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST81	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST82	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST83	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST84	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST85	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST86	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST87	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST88	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST89	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST90	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST91	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST92	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST93	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST94	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST95	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST96	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST97	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST98	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST99	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							
PRPP_MEAST100	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WA)	233-264							



GENE	ALLNOTES	AB Virus (no description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILEBASE	ALLNOTES	VIRUS	122-171	278-279						
PIPA_VACC	SEAL PROTEINASE INHIBITOR 1	VACCINIA VIRUS (STRAIN COPEMAGEN)	11-45							
PTIC1_CMT1	SEAL PROTEINASE INHIBITOR 2 (HOMOLOG FILE)	VACCINIA VIRUS (STRAIN COPEMAGEN)	48-83							
PTAC1_VACC	TYPE II RESTRICTION ENZYME CVAII	PALANCIUM BURBURA CILONELLA VIRUS 1	93-123							
PTAG1_FOMPV	TRANS-ACTIVATOR PROTEIN A3	VACCINIA VIRUS (STRAIN WT. COPEMAGEN AND VACCINIA V1)	3-51							
PTAG2_VACC	TRANS-ACTIVATOR PROTEIN FPI	FOWS FOX VIRUS	3-51							
PTAG3_VARY	TRANS-ACTIVATOR PROTEIN GK1	VACCINIA VIRUS (STRAIN WT. (STRAIN COPEMAGEN))	3-51							
PTAL1_BFDV	TRANS-ACTIVATOR PROTEIN GK1	VACCINIA VIRUS (STRAIN WT. (STRAIN COPEMAGEN))	3-51							
PTAL2_POVBO	LARGE T ANTIGEN	BUDGERIGAR FLEDGLING DISEASE VIRUS	391-331	664-498						
PTAL3_POVNA	LARGE T ANTIGEN	BOVINE POLYOMIA VIRUS	301-337	491-537						
PTAL4_POVVC	LARGE T ANTIGEN	HANISTER POLYOMIA VIRUS	464-501	587-631						
PTAL5_POVLY	LARGE T ANTIGEN	POLYOMIA VIRUS JC	151-187	387-423						
PTAL6_POVAD	LARGE T ANTIGEN	LYMPHOTROPIC POLYOMIA VIRUS	3-41	266-231	417-478					
PTAL7_POVMA	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN J)	509-544							
PTAL8_POVMC	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN A3)	507-542							
PTAL9_POVNA	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	504-539							
PTAL10_POVAD	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN J)	319-378							
PTAL11_POVNA	MIDDLE T ANTIGEN	HANISTER POLYOMIA VIRUS	211-245	388-422						
PTAL12_POVVC	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN A3)	193-236	369-403						
PTAL13_POVBO	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	192-226	369-403						
PTAL14_POVLY	MIDDLE T ANTIGEN	BOVINE POLYOMIA VIRUS	41-83							
PTAL15_NFAC	SMALL T ANTIGEN	BOVINE POLYOMIA VIRUS	3-41							
PTAL16_NFAC	SMALL T ANTIGEN	LYMPHOTROPIC POLYOMIA VIRUS	3-41	48-83						
PTAL17_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMIA VIRUS	608-442	48-83						
PTAL18_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	BOMBYX MORI NUCLEAR POLYOMIA VIRUS	613-497	48-83						
PTAL19_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	OLIGIA PSEUDOTUGATA MULTICAPSID POLYOMIA VIRUS	311-354							
PTAL20_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	SOJAN DUMONDEFFICIENCY VIRUS (AGM155 ISOLATE)	71-109							
PTAL21_NFAC	TAT PROTEIN	SOJAN DUMONDEFFICIENCY VIRUS (ISOLATE AGM / CLONE GR)	121-185							
PTAL22_NFAC	TAT PROTEIN	SOJAN DUMONDEFFICIENCY VIRUS (ISOLATE AGM / CLONE GR)	121-185							
PTAL23_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VIRIA LENTIVIRUS (STRAIN 1314)	28-74							
PTAL24_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VIRIA LENTIVIRUS (STRAIN 1314 / CLONE LVI-1K31)	40-74							
PTAL25_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VIRIA LENTIVIRUS (STRAIN 1314 / CLONE LVI-1K33)	40-74							
PTAL26_NFAC	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	FELINE LEUKAEMIA VIRUS	279-321							
PTAL27_NFAC	T-CELL RECEPTOR BETA CHAIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL28_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL29_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL30_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL31_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL32_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL33_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL34_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL35_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL36_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL37_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL38_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL39_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL40_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL41_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL42_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL43_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL44_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL45_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL46_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL47_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL48_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL49_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL50_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL51_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL52_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL53_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL54_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL55_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL56_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL57_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL58_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL59_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL60_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL61_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL62_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL63_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL64_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL65_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL66_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL67_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL68_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL69_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL70_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL71_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL72_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL73_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL74_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL75_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL76_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL77_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL78_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL79_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL80_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL81_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL82_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL83_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL84_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL85_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL86_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL87_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL88_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL89_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL90_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL91_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL92_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL93_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL94_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL95_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL96_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL97_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL98_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL99_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							
PTAL100_NFAC	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	37-41							



PGCENE	ALLNOTIS	AB Virusess (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
CDLHABIE	ALLNOTIS	VIRUS	493-491	493-538					
PTUN AV131	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 12	210-284						
PTMAF AV154	TRANSFORMING PROTEIN RUN	AVIAN SARCOMA VIRUS (STRAIN 17)	217-288	193-340					
PTOP1 SYPLA	TRANSFORMING PROTEIN MAP	AVIAN MUSCULOPARASITIC FIBROSARCOMA VIRUS A343	127-183	269-310					
PTOP2 AS7B7	DNA TOPOISOMERASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	146-180	481-513	1028-1093	945-979	1122-1163		
PTOP2 AS7B2	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	146-180	480-514	946-978	903-936	1039-1091	1122-1161	
PTIS5 SASAV	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 20V)	146-180	480-514					
PTYST VZVD	PDGF-RELATED TRANSFORMING PROTEIN P18-315	SODAN SARCOMA VIRUS	16-71						
PUBB NCYOP	THYADYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	215-260						
PUBJ1 HCNVA	UBIQUITIN-LIKE PROTEIN	ORGYIA PSEUDOTRUGATA MULTICAPSID POLYHEDROSIS VIRUS	43-80						
PUBJ6 HSNV11	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	169-203						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HGS13)	92-126						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	70-104						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	102-174						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	104-143	113-247					
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (STRAIN B91-4)	216-230						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	36-94	103-141	313-371	314-479			
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	62-170	157-413					
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	90-140	131-194					
PUBJ6 HSNV2H	PROTEIN UL3	HERPESVIRUS SAIMIRI (STRAIN 11)	27-131	350-409					
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	6-50						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	174-208						
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	122-163						
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	67-81	103-237					
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	203-243						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-96	246-283					
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	43-95						
PUBJ6 HSNV2H	PROTEIN UL3	PSEUDORABIES VIRUS (STRAIN NA-3)	61-103						
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	266-300						
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	239-280						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	44-78	421-474					
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	213-233						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-39						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	161-193						
PUBJ6 HSNV2H	PROTEIN UL3	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	253-341	351-399					
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	378-411						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	364-413						
PUBJ6 HSNV2H	PROTEIN UL3	HERPESVIRUS SAIMIRI (STRAIN 11)	29-92	103-231					
PUBJ6 HSNV2H	PROTEIN UL3	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	16-84	163-208					
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	246-285						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	153-187						
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	103-197						
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	102-174						
PUBJ6 HSNV2H	PROTEIN UL3	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47) (STRAIN AB1)	72-108	296-344					
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	94-135	309-353					
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	29-43						
PUBJ6 HSNV2H	PROTEIN UL3	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	139-200						
PUBJ6 HSNV2H	PROTEIN UL3	EPSTEIN-BARR VIRUS (STRAIN B95-4)	113-147						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-231						
PUBJ6 HSNV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	231-268						
PUBJ6 HSNV2H	PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)							



80



PCGENE	ALLNOTES	AE Virus (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PUS01 HCV1	HYPOTHEICAL PROTEIN HCV1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	84-125							
PUS02 HCV2	URACIL-DNA GLYCOSYLASE	HEPES SIMPLEX VIRUS (TYPE 1) (STRAIN 17)	227-264							
PUS03 HCV3	URACIL-DNA GLYCOSYLASE	HEPES SIMPLEX VIRUS (TYPE 2) (STRAIN 32)	188-219							
PUS04 HCV4	URACIL-DNA GLYCOSYLASE	HEPES SIMPLEX VIRUS (TYPE 3) (STRAIN 1053)	148-189							
PUS05 HCV5	URACIL-DNA GLYCOSYLASE	HEPESVIRUS SANGUI (STRAIN 13)	135-176							
PUS06 HCV6	URACIL-DNA GLYCOSYLASE	SHOE FIBROMA VIRUS (STRAIN KASZA)	81-113							
PUS07 HCV7	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	79-120							
PUS08 HCV8	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	84-120							
PUS09 HCV9	URACIL-DNA GLYCOSYLASE		2-16							
PUS10 HCV10	HYPOTHEICAL PROTEIN HCV10	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)								
PUS11 HCV11	HYPOTHEICAL PROTEIN HCV11	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	3-51							
PUS12 HCV12	HYPOTHEICAL PROTEIN HCV12	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-225							
PUS13 HCV13	MEMBRANE PROTEIN HCV13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	284-335							
PUS14 HCV14	HYPOTHEICAL PROTEIN HCV14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-172							
PUS15 HCV15	HYPOTHEICAL PROTEIN HCV15	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	335-384							
PUS16 HCV16	HYPOTHEICAL PROTEIN HCV16	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40							
PUS17 HCV17	G-PROTEIN COUPLED RECEPTOR HOMOLOG US37	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-169							
PUS18 HCV18	HYPOTHEICAL PROTEIN HCV18	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-52							
PUS19 HCV19	HELICASE	ALFA Mosaic Virus (STRAIN 4317) ISOLATE LEIDEN	313-350							
PUS20 HCV20	HELICASE	AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	15-117							
PUS21 HCV21	HELICASE	TOBACCO RATTLE VIRUS (STRAIN PSC)	21-55							
PUS22 HCV22	HELICASE	BROAD BEAN MOTTLE VIRUS	21-55							
PUS23 HCV23	HELICASE	BROME MOSAIC VIRUS	4-46							
PUS24 HCV24	HELICASE	COMPEA CHLOROTIC MOTTLE VIRUS	4-53							
PUS25 HCV25	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	11-44							
PUS26 HCV26	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN O)	11-44							
PUS27 HCV27	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN Q)	11-44							
PUS28 HCV28	HELICASE	PEANUT STUNT VIRUS (STRAIN J)	4-46							
PUS29 HCV29	HELICASE	TOMATO ASPERMY VIRUS	11-59							
PUS30 HCV30	HELICASE	TURKEY HERPESVIRUS (STRAIN 12)	177-211							
PUS31 HCV31	HELICASE	BODNA DISEASE VIRUS	63-121							
PUS32 HCV32	HELICASE	AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	4-50							
PUS33 HCV33	HELICASE	POTATO LEAFROLL VIRUS (STRAIN 1)	116-150							
PUS34 HCV34	HELICASE	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	116-150							
PUS35 HCV35	HELICASE	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS36 HCV36	HELICASE	EARLY BROWNING VIRUS	115-192							
PUS37 HCV37	HELICASE	TOBACCO RATTLE VIRUS (STRAIN SYD. AND (STRAIN PSC)	187-201							
PUS38 HCV38	HELICASE	TOBACCO RATTLE VIRUS (STRAIN TCM)	43-79							
PUS39 HCV39	HELICASE	COMPEA CHLOROTIC MOTTLE VIRUS	788-806							
PUS40 HCV40	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	184-420							
PUS41 HCV41	HELICASE	PEANUT STUNT VIRUS (STRAIN J)	217-251							
PUS42 HCV42	HELICASE	TOMATO ASPERMY VIRUS	722-754							
PUS43 HCV43	HELICASE	TOBACCO RATTLE VIRUS (STRAIN TCM)	103-218							
PUS44 HCV44	HELICASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	93-97							
PUS45 HCV45	HELICASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	54-102							
PUS46 HCV46	HELICASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	151-199							
PUS47 HCV47	HELICASE	BROME MOSAIC VIRUS	11-45							
PUS48 HCV48	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	215-253							
PUS49 HCV49	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN N)	215-253							
PUS50 HCV50	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN O)	215-253							
PUS51 HCV51	HELICASE	CUCUMBER MOSAIC VIRUS (STRAIN V)	215-253							



82



[illegible]



84



PCGENE	ALLNOTES	ALL NAMES (see bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PROTEIN E3	PROTEIN E3	VAROLIA VIRUS	17-41					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	38-93					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS (STRAIN DAIKEN I)	38-103					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS (STRAIN WA)	38-103					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS	38-103					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	105-139	332-344				
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS (STRAIN WA)	105-139	332-344				
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS	105-139	367-401				
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS	112-163					
PROTEIN E3	PROTEIN E3	VACCINIA VIRUS	137-171					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 1A	56-90					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 31	31-47	132-167				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 31	56-90					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 31	59-96					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 31	59-96	312-344				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 41	31-47					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 42	31-47	119-174				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 42	31-47					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 48	365-399					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 48	174-210					
PROTEIN E3	PROTEIN E3	EUROPEAN ELK PAPILLOMA VIRUS	72-117					
PROTEIN E3	PROTEIN E3	AUTOGRAHA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	342-383	437-471				
PROTEIN E3	PROTEIN E3	COTTONTAIL BABBIE (SHORE) PAPILLOMA VIRUS (STRAIN KANSAS)	5-37	274-310				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 5	5-37	169-182				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 8	5-37	315-349				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 16	81-105					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 16	81-105	159-192				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 1A	81-105	159-192				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 2A	81-105	159-192				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 31	81-105	297-331				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 33	81-105					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 33	81-105	159-192				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 33	81-105	232-257				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 39	74-110					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 41	6-54					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 41	5-53	168-182				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 47	154-191					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 51	13-47	179-213				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 57	2-36					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 59	5-53					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 59	107-141					
PROTEIN E3	PROTEIN E3	DEER PAPILLOMA VIRUS	113-150					
PROTEIN E3	PROTEIN E3	EUROPEAN ELK PAPILLOMA VIRUS	318-361					
PROTEIN E3	PROTEIN E3	PYGMY CHIMPANZEE PAPILLOMA VIRUS TYPE 1	42-106	307-341				
PROTEIN E3	PROTEIN E3	MUSKUS PAPILLOMA VIRUS TYPE 1	26-37					
PROTEIN E3	PROTEIN E3	AUTOGRAHA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	119-156					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 41	61-97					
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 41	3-40	96-130				
PROTEIN E3	PROTEIN E3	HUMAN PAPILLOMA VIRUS TYPE 59	481-519					
PROTEIN E3	PROTEIN E3	TRICHOPUS NIGRUS GRANULOSUS VIRUS (THGV)	195-229					
PROTEIN E3	PROTEIN E3	BEAR VIRUS (REV)	318-361					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYEDROSIS VIRUS	42-86					
PROTEIN E3	PROTEIN E3	ORGYIA PSEUDOTSUGATA MULTIC						



86



Accession	Gene	Protein	Virus	Area1	Area2	Area3	Area4	Area5	Area6
AF010001	ALL-PROTEIN	ALL-PROTEIN	ALL-PROTEIN						
AF010002	PROTEIN	PROTEIN	PROTEIN						
AF010003	PROTEIN	PROTEIN	PROTEIN						
AF010004	PROTEIN	PROTEIN	PROTEIN						
AF010005	PROTEIN	PROTEIN	PROTEIN						
AF010006	PROTEIN	PROTEIN	PROTEIN						
AF010007	PROTEIN	PROTEIN	PROTEIN						
AF010008	PROTEIN	PROTEIN	PROTEIN						
AF010009	PROTEIN	PROTEIN	PROTEIN						
AF010010	PROTEIN	PROTEIN	PROTEIN						
AF010011	PROTEIN	PROTEIN	PROTEIN						
AF010012	PROTEIN	PROTEIN	PROTEIN						
AF010013	PROTEIN	PROTEIN	PROTEIN						
AF010014	PROTEIN	PROTEIN	PROTEIN						
AF010015	PROTEIN	PROTEIN	PROTEIN						
AF010016	PROTEIN	PROTEIN	PROTEIN						
AF010017	PROTEIN	PROTEIN	PROTEIN						
AF010018	PROTEIN	PROTEIN	PROTEIN						
AF010019	PROTEIN	PROTEIN	PROTEIN						
AF010020	PROTEIN	PROTEIN	PROTEIN						
AF010021	PROTEIN	PROTEIN	PROTEIN						
AF010022	PROTEIN	PROTEIN	PROTEIN						
AF010023	PROTEIN	PROTEIN	PROTEIN						
AF010024	PROTEIN	PROTEIN	PROTEIN						
AF010025	PROTEIN	PROTEIN	PROTEIN						
AF010026	PROTEIN	PROTEIN	PROTEIN						
AF010027	PROTEIN	PROTEIN	PROTEIN						
AF010028	PROTEIN	PROTEIN	PROTEIN						
AF010029	PROTEIN	PROTEIN	PROTEIN						
AF010030	PROTEIN	PROTEIN	PROTEIN						
AF010031	PROTEIN	PROTEIN	PROTEIN						
AF010032	PROTEIN	PROTEIN	PROTEIN						
AF010033	PROTEIN	PROTEIN	PROTEIN						
AF010034	PROTEIN	PROTEIN	PROTEIN						
AF010035	PROTEIN	PROTEIN	PROTEIN						
AF010036	PROTEIN	PROTEIN	PROTEIN						
AF010037	PROTEIN	PROTEIN	PROTEIN						
AF010038	PROTEIN	PROTEIN	PROTEIN						
AF010039	PROTEIN	PROTEIN	PROTEIN						
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AF010056	PROTEIN	PROTEIN	PROTEIN						
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AF010063	PROTEIN	PROTEIN	PROTEIN						
AF010064	PROTEIN	PROTEIN	PROTEIN						
AF010065	PROTEIN	PROTEIN	PROTEIN						
AF010066	PROTEIN	PROTEIN	PROTEIN						
AF010067	PROTEIN	PROTEIN	PROTEIN						
AF010068	PROTEIN	PROTEIN	PROTEIN						
AF010069	PROTEIN	PROTEIN	PROTEIN						
AF010070	PROTEIN	PROTEIN	PROTEIN						
AF010071	PROTEIN	PROTEIN	PROTEIN						
AF010072	PROTEIN	PROTEIN	PROTEIN						
AF010073	PROTEIN	PROTEIN	PROTEIN						
AF010074	PROTEIN	PROTEIN	PROTEIN						
AF010075	PROTEIN	PROTEIN	PROTEIN						
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AF010092	PROTEIN	PROTEIN	PROTEIN						
AF010093	PROTEIN	PROTEIN	PROTEIN						
AF010094	PROTEIN	PROTEIN	PROTEIN						
AF010095	PROTEIN	PROTEIN	PROTEIN						
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AF010097	PROTEIN	PROTEIN	PROTEIN						
AF010098	PROTEIN	PROTEIN	PROTEIN						
AF010099	PROTEIN	PROTEIN	PROTEIN						
AF010100	PROTEIN	PROTEIN	PROTEIN						
AF010101	PROTEIN	PROTEIN	PROTEIN						
AF010102	PROTEIN	PROTEIN	PROTEIN						
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AF010171	PROTEIN	PROTEIN	PROTEIN						
AF010172	PROTEIN	PROTEIN	PROTEIN						
AF010173	PROTEIN	PROTEIN	PROTEIN						
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AF010190	PROTEIN	PROTEIN	PROTEIN						
AF010191	PROTEIN	PROTEIN	PROTEIN						
AF010192	PROTEIN	PROTEIN	PROTEIN						
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GENE	ALLIOTIS	AD Virus (see bacteriophage)	ADV-1	ADV-2	ADV-3	ADV-4	ADV-5	ADV-6	ADV-7	ADV-8	ADV-9	ADV-10	ADV-11	ADV-12	ADV-13	ADV-14	ADV-15	ADV-16	ADV-17	ADV-18	ADV-19	ADV-20	ADV-21	ADV-22	ADV-23	ADV-24	ADV-25	ADV-26	ADV-27	ADV-28	ADV-29	ADV-30	ADV-31	ADV-32	ADV-33	ADV-34	ADV-35	ADV-36	ADV-37	ADV-38	ADV-39	ADV-40	ADV-41	ADV-42	ADV-43	ADV-44	ADV-45	ADV-46	ADV-47	ADV-48	ADV-49	ADV-50	ADV-51	ADV-52	ADV-53	ADV-54	ADV-55	ADV-56	ADV-57	ADV-58	ADV-59	ADV-60	ADV-61	ADV-62	ADV-63	ADV-64	ADV-65	ADV-66	ADV-67	ADV-68	ADV-69	ADV-70	ADV-71	ADV-72	ADV-73	ADV-74	ADV-75	ADV-76	ADV-77	ADV-78	ADV-79	ADV-80	ADV-81	ADV-82	ADV-83	ADV-84	ADV-85	ADV-86	ADV-87	ADV-88	ADV-89	ADV-90	ADV-91	ADV-92	ADV-93	ADV-94	ADV-95	ADV-96	ADV-97	ADV-98	ADV-99	ADV-100	ADV-101	ADV-102	ADV-103	ADV-104	ADV-105	ADV-106	ADV-107	ADV-108	ADV-109	ADV-110	ADV-111	ADV-112	ADV-113	ADV-114	ADV-115	ADV-116	ADV-117	ADV-118	ADV-119	ADV-120	ADV-121	ADV-122	ADV-123	ADV-124	ADV-125	ADV-126	ADV-127	ADV-128	ADV-129	ADV-130	ADV-131	ADV-132	ADV-133	ADV-134	ADV-135	ADV-136	ADV-137	ADV-138	ADV-139	ADV-140	ADV-141	ADV-142	ADV-143	ADV-144	ADV-145	ADV-146	ADV-147	ADV-148	ADV-149	ADV-150	ADV-151	ADV-152	ADV-153	ADV-154	ADV-155	ADV-156	ADV-157	ADV-158	ADV-159	ADV-160	ADV-161	ADV-162	ADV-163	ADV-164	ADV-165	ADV-166	ADV-167	ADV-168	ADV-169	ADV-170	ADV-171	ADV-172	ADV-173	ADV-174	ADV-175	ADV-176	ADV-177	ADV-178	ADV-179	ADV-180	ADV-181	ADV-182	ADV-183	ADV-184	ADV-185	ADV-186	ADV-187	ADV-188	ADV-189	ADV-190	ADV-191	ADV-192	ADV-193	ADV-194	ADV-195	ADV-196	ADV-197	ADV-198	ADV-199	ADV-200	ADV-201	ADV-202	ADV-203	ADV-204	ADV-205	ADV-206	ADV-207	ADV-208	ADV-209	ADV-210	ADV-211	ADV-212	ADV-213	ADV-214	ADV-215	ADV-216	ADV-217	ADV-218	ADV-219	ADV-220	ADV-221	ADV-222	ADV-223	ADV-224	ADV-225	ADV-226	ADV-227	ADV-228	ADV-229	ADV-230	ADV-231	ADV-232	ADV-233	ADV-234	ADV-235	ADV-236	ADV-237	ADV-238	ADV-239	ADV-240	ADV-241	ADV-242	ADV-243	ADV-244	ADV-245	ADV-246	ADV-247	ADV-248	ADV-249	ADV-250	ADV-251	ADV-252	ADV-253	ADV-254	ADV-255	ADV-256	ADV-257	ADV-258	ADV-259	ADV-260	ADV-261	ADV-262	ADV-263	ADV-264	ADV-265	ADV-266	ADV-267	ADV-268	ADV-269	ADV-270	ADV-271	ADV-272	ADV-273	ADV-274	ADV-275	ADV-276	ADV-277	ADV-278	ADV-279	ADV-280	ADV-281	ADV-282	ADV-283	ADV-284	ADV-285	ADV-286	ADV-287	ADV-288	ADV-289	ADV-290	ADV-291	ADV-292	ADV-293	ADV-294	ADV-295	ADV-296	ADV-297	ADV-298	ADV-299	ADV-300	ADV-301	ADV-302	ADV-303	ADV-304	ADV-305	ADV-306	ADV-307	ADV-308	ADV-309	ADV-310	ADV-311	ADV-312	ADV-313	ADV-314	ADV-315	ADV-316	ADV-317	ADV-318	ADV-319	ADV-320	ADV-321	ADV-322	ADV-323	ADV-324	ADV-325	ADV-326	ADV-327	ADV-328	ADV-329	ADV-330	ADV-331	ADV-332	ADV-333	ADV-334	ADV-335	ADV-336	ADV-337	ADV-338	ADV-339	ADV-340	ADV-341	ADV-342	ADV-343	ADV-344	ADV-345	ADV-346	ADV-347	ADV-348	ADV-349	ADV-350	ADV-351	ADV-352	ADV-353	ADV-354	ADV-355	ADV-356	ADV-357	ADV-358	ADV-359	ADV-360	ADV-361	ADV-362	ADV-363	ADV-364	ADV-365	ADV-366	ADV-367	ADV-368	ADV-369	ADV-370	ADV-371	ADV-372	ADV-373	ADV-374	ADV-375	ADV-376	ADV-377	ADV-378	ADV-379	ADV-380	ADV-381	ADV-382	ADV-383	ADV-384	ADV-385	ADV-386	ADV-387	ADV-388	ADV-389	ADV-390	ADV-391	ADV-392	ADV-393	ADV-394	ADV-395	ADV-396	ADV-397	ADV-398	ADV-399	ADV-400	ADV-401	ADV-402	ADV-403	ADV-404	ADV-405	ADV-406	ADV-407	ADV-408	ADV-409	ADV-410	ADV-411	ADV-412	ADV-413	ADV-414	ADV-415	ADV-416	ADV-417	ADV-418	ADV-419	ADV-420	ADV-421	ADV-422	ADV-423	ADV-424	ADV-425	ADV-426	ADV-427	ADV-428	ADV-429	ADV-430	ADV-431	ADV-432	ADV-433	ADV-434	ADV-435	ADV-436	ADV-437	ADV-438	ADV-439	ADV-440	ADV-441	ADV-442	ADV-443	ADV-444	ADV-445	ADV-446	ADV-447	ADV-448	ADV-449	ADV-450	ADV-451	ADV-452	ADV-453	ADV-454	ADV-455	ADV-456	ADV-457	ADV-458	ADV-459	ADV-460	ADV-461	ADV-462	ADV-463	ADV-464	ADV-465	ADV-466	ADV-467	ADV-468	ADV-469	ADV-470	ADV-471	ADV-472	ADV-473	ADV-474	ADV-475	ADV-476	ADV-477	ADV-478	ADV-479	ADV-480	ADV-481	ADV-482	ADV-483	ADV-484	ADV-485	ADV-486	ADV-487	ADV-488	ADV-489	ADV-490	ADV-491	ADV-492	ADV-493	ADV-494	ADV-495	ADV-496	ADV-497	ADV-498	ADV-499	ADV-500	ADV-501	ADV-502	ADV-503	ADV-504	ADV-505	ADV-506	ADV-507	ADV-508	ADV-509	ADV-510	ADV-511	ADV-512	ADV-513	ADV-514	ADV-515	ADV-516	ADV-517	ADV-518	ADV-519	ADV-520	ADV-521	ADV-522	ADV-523	ADV-524	ADV-525	ADV-526	ADV-527	ADV-528	ADV-529	ADV-530	ADV-531	ADV-532	ADV-533	ADV-534	ADV-535	ADV-536	ADV-537	ADV-538	ADV-539	ADV-540	ADV-541	ADV-542	ADV-543	ADV-544	ADV-545	ADV-546	ADV-547	ADV-548	ADV-549	ADV-550	ADV-551	ADV-552	ADV-553	ADV-554	ADV-555	ADV-556	ADV-557	ADV-558	ADV-559	ADV-560	ADV-561	ADV-562	ADV-563	ADV-564	ADV-565	ADV-566	ADV-567	ADV-568	ADV-569	ADV-570	ADV-571	ADV-572	ADV-573	ADV-574	ADV-575	ADV-576	ADV-577	ADV-578	ADV-579	ADV-580	ADV-581	ADV-582	ADV-583	ADV-584	ADV-585	ADV-586	ADV-587	ADV-588	ADV-589	ADV-590	ADV-591	ADV-592	ADV-593	ADV-594	ADV-595	ADV-596	ADV-597	ADV-598	ADV-599	ADV-600	ADV-601	ADV-602	ADV-603	ADV-604	ADV-605	ADV-606	ADV-607	ADV-608	ADV-609	ADV-610	ADV-611	ADV-612	ADV-613	ADV-614	ADV-615	ADV-616	ADV-617	ADV-618	ADV-619	ADV-620	ADV-621	ADV-622	ADV-623	ADV-624	ADV-625	ADV-626	ADV-627	ADV-628	ADV-629	ADV-630	ADV-631	ADV-632	ADV-633	ADV-634	ADV-635	ADV-636	ADV-637	ADV-638	ADV-639	ADV-640	ADV-641	ADV-642	ADV-643	ADV-644	ADV-645	ADV-646	ADV-647	ADV-648	ADV-649	ADV-650	ADV-651	ADV-652	ADV-653	ADV-654	ADV-655	ADV-656	ADV-657	ADV-658	ADV-659	ADV-660	ADV-661	ADV-662	ADV-663	ADV-664	ADV-665	ADV-666	ADV-667	ADV-668	ADV-669	ADV-670	ADV-671	ADV-672	ADV-673	ADV-674	ADV-675	ADV-676	ADV-677	ADV-678	ADV-679	ADV-680	ADV-681	ADV-682	ADV-683	ADV-684	ADV-685	ADV-686	ADV-687	ADV-688	ADV-689	ADV-690	ADV-691	ADV-692	ADV-693	ADV-694	ADV-695	ADV-696	ADV-697	ADV-698	ADV-699	ADV-700	ADV-701	ADV-702	ADV-703	ADV-704	ADV-705	ADV-706	ADV-707	ADV-708	ADV-709	ADV-710	ADV-711	ADV-712	ADV-713	ADV-714	ADV-715	ADV-716	ADV-717	ADV-718	ADV-719	ADV-720	ADV-721	ADV-722	ADV-723	ADV-724	ADV-725	ADV-726	ADV-727	ADV-728	ADV-729	ADV-730	ADV-731	ADV-732	ADV-733	ADV-734	ADV-735	ADV-736	ADV-737	ADV-738	ADV-739	ADV-740	ADV-741	ADV-742	ADV-743	ADV-744	ADV-745	ADV-746	ADV-747	ADV-748	ADV-749	ADV-750	ADV-751	ADV-752	ADV-753	ADV-754	ADV-755	ADV-756	ADV-757	ADV-758	ADV-759	ADV-760	ADV-761	ADV-762	ADV-763	ADV-764	ADV-765	ADV-766	ADV-767	ADV-768	ADV-769	ADV-770	ADV-771	ADV-772	ADV-773	ADV-774	ADV-775	ADV-776	ADV-777	ADV-778	ADV-779	ADV-780	ADV-781	ADV-782	ADV-783	ADV-784	ADV-785	ADV-786	ADV-787	ADV-788	ADV-789	ADV-790	ADV-791	ADV-792	ADV-793	ADV-794	ADV-795	ADV-796	ADV-797	ADV-798	ADV-799	ADV-800	ADV-801	ADV-802	ADV-803	ADV-804	ADV-805	ADV-806	ADV-807	ADV-808	ADV-809	ADV-810	ADV-811	ADV-812	ADV-813	ADV-814	ADV-815	ADV-816	ADV-817	ADV-818	ADV-819	ADV-820	ADV-821	ADV-822	ADV-823	ADV-824	ADV-825	ADV-826	ADV-827	ADV-828	ADV-829	ADV-830	ADV-831	ADV-832	ADV-833	ADV-834	ADV-835	ADV-836	ADV-837	ADV-838	ADV-839	ADV-840	ADV-841	ADV-842	ADV-843	ADV-844	ADV-845	ADV-846	ADV-847	ADV-848	ADV-849	ADV-850	ADV-851	ADV-852	ADV-853	ADV-854	ADV-855	ADV-856	ADV-857	ADV-858	ADV-859	ADV-860	ADV-861	ADV-862	ADV-863	ADV-864	ADV-865	ADV-866	ADV-867	ADV-868	ADV-869	ADV-870	ADV-871	ADV-872	ADV-873	ADV-874	ADV-875	ADV-876	ADV-877	ADV-878	ADV-879	ADV-880	ADV-881	ADV-882	ADV-883	ADV-884	ADV-885	ADV-886	ADV-887	ADV-888	ADV-889	ADV-890	ADV-891	ADV-892	ADV-893	ADV-894	ADV-895	ADV-896	ADV-897	ADV-898	ADV-899	ADV-900	ADV-901	ADV-902	ADV-903	ADV-904	ADV-905	ADV-906	ADV-907	ADV-908	ADV-909	ADV-910	ADV-911	ADV-912	ADV-913	ADV-914	ADV-915	ADV-916	ADV-917	ADV-918	ADV-919	ADV-920	ADV-921	ADV-922	ADV-923	ADV-924	ADV-925	ADV-926	ADV-927	ADV-928	ADV-929	ADV-930	ADV-931	ADV-932	ADV-933	ADV-934	ADV-935	ADV-936	ADV-937	ADV-938	ADV-939	ADV-940	ADV-941	ADV-942	ADV-943	ADV-944	ADV-945	ADV-946	ADV-947	ADV-948	ADV-949	ADV-950	ADV-951	ADV-952	ADV-953	ADV-954	ADV-955	ADV-956	ADV-957	ADV-958	ADV-959	ADV-960	ADV-961	ADV-962	ADV-963	ADV-964	ADV-965	ADV-966	ADV-967	ADV-968	ADV-969	ADV-970	ADV-971	ADV-972	ADV-973	ADV-974	ADV-975	ADV-976	ADV-977	ADV-978	ADV-979	ADV-980	ADV-981	ADV-982	ADV-983	ADV-984	ADV-985	ADV-986	ADV-987	ADV-988	ADV-989	ADV-990	ADV-991	ADV-992	ADV-993	ADV-994	ADV-995	ADV-996	ADV-997	ADV-998	ADV-999	ADV-1000
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102



GENE	ALLNOTES	VIRUS (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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104



GENE	FUNCTION	PROTEIN	PROTEIN (see description page)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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[illegible]



**TABLE VI**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS**



108



GENE	1991-2004	All Viruses (see RestrictionMap)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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		(07-12-14)		All Viruses (not bacteriophage phage)		AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE	PCGENE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			



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1911-1914	1915-1918	1919-1922	1923-1926	1927-1930	1931-1934	1935-1938	1939-1942	1943-1946	1947-1950	1951-1954	1955-1958	1959-1962	1963-1966	1967-1970	1971-1974	1975-1978	1979-1982	1983-1986	1987-1990	1991-1994	1995-1998	1999-2002	2003-2006	2007-2010	2011-2014	2015-2018	2019-2022	2023-2026	2027-2030	2031-2034	2035-2038	2039-2042	2043-2046	2047-2050	2051-2054	2055-2058	2059-2062	2063-2066	2067-2070	2071-2074	2075-2078	2079-2082	2083-2086	2087-2090	2091-2094	2095-2098	2099-2102	2103-2106	2107-2110	2111-2114	2115-2118	2119-2122	2123-2126	2127-2130	2131-2134	2135-2138	2139-2142	2143-2146	2147-2150	2151-2154	2155-2158	2159-2162	2163-2166	2167-2170	2171-2174	2175-2178	2179-2182	2183-2186	2187-2190	2191-2194	2195-2198	2199-2202	2203-2206	2207-2210	2211-2214	2215-2218	2219-2222	2223-2226	2227-2230	2231-2234	2235-2238	2239-2242	2243-2246	2247-2250	2251-2254	2255-2258	2259-2262	2263-2266	2267-2270	2271-2274	2275-2278	2279-2282	2283-2286	2287-2290	2291-2294	2295-2298	2299-2302	2303-2306	2307-2310	2311-2314	2315-2318	2319-2322	2323-2326	2327-2330	2331-2334	2335-2338	2339-2342	2343-2346	2347-2350	2351-2354	2355-2358	2359-2362	2363-2366	2367-2370	2371-2374	2375-2378	2379-2382	2383-2386	2387-2390	2391-2394	2395-2398	2399-2402	2403-2406	2407-2410	2411-2414	2415-2418	2419-2422	2423-2426	2427-2430	2431-2434	2435-2438	2439-2442	2443-2446	2447-2450	2451-2454	2455-2458	2459-2462	2463-2466	2467-2470	2471-2474	2475-2478	2479-2482	2483-2486	2487-2490	2491-2494	2495-2498	2499-2502	2503-2506	2507-2510	2511-2514	2515-2518	2519-2522	2523-2526	2527-2530	2531-2534	2535-2538	2539-2542	2543-2546	2547-2550	2551-2554	2555-2558	2559-2562	2563-2566	2567-2570	2571-2574	2575-2578	2579-2582	2583-2586	2587-2590	2591-2594	2595-2598	2599-2602	2603-2606	2607-2610	2611-2614	2615-2618	2619-2622	2623-2626	2627-2630	2631-2634	2635-2638	2639-2642	2643-2646	2647-2650	2651-2654	2655-2658	2659-2662	2663-2666	2667-2670	2671-2674	2675-2678	2679-2682	2683-2686	2687-2690	2691-2694	2695-2698	2699-2702	2703-2706	2707-2710	2711-2714	2715-2718	2719-2722	2723-2726	2727-2730	2731-2734	2735-2738	2739-2742	2743-2746	2747-2750	2751-2754	2755-2758	2759-2762	2763-2766	2767-2770	2771-2774	2775-2778	2779-2782	2783-2786	2787-2790	2791-2794	2795-2798	2799-2802	2803-2806	2807-2810	2811-2814	2815-2818	2819-2822	2823-2826	2827-2830	2831-2834	2835-2838	2839-2842	2843-2846	2847-2850	2851-2854	2855-2858	2859-2862	2863-2866	2867-2870	2871-2874	2875-2878	2879-2882	2883-2886	2887-2890	2891-2894	2895-2898	2899-2902	2903-2906	2907-2910	2911-2914	2915-2918	2919-2922	2923-2926	2927-2930	2931-2934	2935-2938	2939-2942	2943-2946	2947-2950	2951-2954	2955-2958	2959-2962	2963-2966	2967-2970	2971-2974	2975-2978	2979-2982	2983-2986	2987-2990	2991-2994	2995-2998	29
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118



GENE	1975-1984	All Viruses (as determined)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCG CODE		Virus		AREA 1		AREA 2		AREA 3		AREA 4		AREA 5		AREA 6		AREA 7		AREA 8		AREA 9		AREA 10		AREA 11		AREA 12		AREA 13		AREA 14		AREA 15		AREA 16		AREA 17		AREA 18		AREA 19		AREA 20		AREA 21		AREA 22		AREA 23		AREA 24		AREA 25		AREA 26		AREA 27		AREA 28		AREA 29		AREA 30		AREA 31		AREA 32		AREA 33		AREA 34		AREA 35		AREA 36		AREA 37		AREA 38		AREA 39		AREA 40		AREA 41		AREA 42		AREA 43		AREA 44		AREA 45		AREA 46		AREA 47		AREA 48		AREA 49		AREA 50		AREA 51		AREA 52		AREA 53		AREA 54		AREA 55		AREA 56		AREA 57		AREA 58		AREA 59		AREA 60		AREA 61		AREA 62		AREA 63		AREA 64		AREA 65		AREA 66		AREA 67		AREA 68		AREA 69		AREA 70		AREA 71		AREA 72		AREA 73		AREA 74		AREA 75		AREA 76		AREA 77		AREA 78		AREA 79		AREA 80		AREA 81		AREA 82		AREA 83		AREA 84		AREA 85		AREA 86		AREA 87		AREA 88		AREA 89		AREA 90		AREA 91		AREA 92		AREA 93		AREA 94		AREA 95		AREA 96		AREA 97		AREA 98		AREA 99		AREA 100		AREA 101		AREA 102		AREA 103		AREA 104		AREA 105		AREA 106		AREA 107		AREA 108		AREA 109		AREA 110		AREA 111		AREA 112		AREA 113		AREA 114		AREA 115		AREA 116		AREA 117		AREA 118		AREA 119		AREA 120		AREA 121		AREA 122		AREA 123		AREA 124		AREA 125		AREA 126		AREA 127		AREA 128		AREA 129		AREA 130		AREA 131		AREA 132		AREA 133		AREA 134		AREA 135		AREA 136		AREA 137		AREA 138		AREA 139		AREA 140		AREA 141		AREA 142		AREA 143		AREA 144		AREA 145		AREA 146		AREA 147		AREA 148		AREA 149		AREA 150		AREA 151		AREA 152		AREA 153		AREA 154		AREA 155		AREA 156		AREA 157		AREA 158		AREA 159		AREA 160		AREA 161		AREA 162		AREA 163		AREA 164		AREA 165		AREA 166		AREA 167		AREA 168		AREA 169		AREA 170		AREA 171		AREA 172		AREA 173		AREA 174		AREA 175		AREA 176		AREA 177		AREA 178		AREA 179		AREA 180		AREA 181		AREA 182		AREA 183		AREA 184		AREA 185		AREA 186		AREA 187		AREA 188		AREA 189		AREA 190		AREA 191		AREA 192		AREA 193		AREA 194		AREA 195		AREA 196		AREA 197		AREA 198		AREA 199		AREA 200		AREA 201		AREA 202		AREA 203		AREA 204		AREA 205		AREA 206		AREA 207		AREA 208		AREA 209		AREA 210		AREA 211		AREA 212		AREA 213		AREA 214		AREA 215		AREA 216		AREA 217		AREA 218		AREA 219		AREA 220		AREA 221		AREA 222		AREA 223		AREA 224		AREA 225		AREA 226		AREA 227		AREA 228		AREA 229		AREA 230		AREA 231		AREA 232		AREA 233		AREA 234		AREA 235		AREA 236		AREA 237		AREA 238		AREA 239		AREA 240		AREA 241		AREA 242		AREA 243		AREA 244		AREA 245		AREA 246		AREA 247		AREA 248		AREA 249		AREA 250		AREA 251		AREA 252		AREA 253		AREA 254		AREA 255		AREA 256		AREA 257		AREA 258		AREA 259		AREA 260		AREA 261		AREA 262		AREA 263		AREA 264		AREA 265		AREA 266		AREA 267		AREA 268		AREA 269		AREA 270		AREA 271		AREA 272		AREA 273		AREA 274		AREA 275		AREA 276		AREA 277		AREA 278		AREA 279		AREA 280		AREA 281		AREA 282		AREA 283		AREA 284		AREA 285		AREA 286		AREA 287		AREA 288		AREA 289		AREA 290		AREA 291		AREA 292		AREA 293		AREA 294		AREA 295		AREA 296		AREA 297		AREA 298		AREA 299		AREA 300		AREA 301		AREA 302		AREA 303		AREA 304		AREA 305		AREA 306		AREA 307		AREA 308		AREA 309		AREA 310		AREA 311		AREA 312		AREA 313		AREA 314		AREA 315		AREA 316		AREA 317		AREA 318		AREA 319		AREA 320		AREA 321		AREA 322		AREA 323		AREA 324		AREA 325		AREA 326		AREA 327		AREA 328		AREA 329		AREA 330		AREA 331		AREA 332		AREA 333		AREA 334		AREA 335		AREA 336		AREA 337		AREA 338		AREA 339		AREA 340		AREA 341		AREA 342		AREA 343		AREA 344		AREA 345		AREA 346		AREA 347		AREA 348		AREA 349		AREA 350		AREA 351		AREA 352		AREA 353		AREA 354		AREA 355		AREA 356		AREA 357		AREA 358		AREA 359		AREA 360		AREA 361		AREA 362		AREA 363		AREA 364		AREA 365		AREA 366		AREA 367		AREA 368		AREA 369		AREA 370		AREA 371		AREA 372		AREA 373		AREA 374		AREA 375		AREA 376		AREA 377		AREA 378		AREA 379		AREA 380		AREA 381		AREA 382		AREA 383		AREA 384		AREA 385		AREA 386		AREA 387		AREA 388		AREA 389		AREA 390		AREA 391		AREA 392		AREA 393		AREA 394		AREA 395		AREA 396		AREA 397		AREA 398		AREA 399		AREA 400		AREA 401		AREA 402		AREA 403		AREA 404		AREA 405		AREA 406		AREA 407		AREA 408		AREA 409		AREA 410		AREA 411		AREA 412		AREA 413		AREA 414		AREA 415		AREA 416		AREA 417		AREA 418		AREA 419		AREA 420		AREA 421		AREA 422		AREA 423		AREA 424		AREA 425		AREA 426		AREA 427		AREA 428		AREA 429		AREA 430		AREA 431		AREA 432		AREA 433		AREA 434		AREA 435		AREA 436		AREA 437		AREA 438		AREA 439		AREA 440	
PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PRO																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												



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128



PCGENE	IP1717a.4	ALL Viruses (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PV001 SVYKA	PROTEIN C1	SHOPE FIBROMA VIRUS (STRAIN KASZA)	209-216							
PV002 SVYKA	PROTEIN C2	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-46							
PV003 SVYKA	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	12-46							
PV004 SVYKA	PROTEIN C4	VARIOLA VIRUS	152-179							
PV005 SVYKA	HYPOPHARYNGEAL PROTEIN C5	SHOPE FIBROMA VIRUS (STRAIN KASZA)	95-133							
PV006 SVYKA	PROTEIN C6	VACCINIA VIRUS (STRAIN COPENHAGEN)	18-43							
PV007 SVYKA	PROTEIN C7	VACCINIA VIRUS (STRAIN WR)	18-43							
PV008 SVYKA	PROTEIN C8	VARIOLA VIRUS	16-111							
PV009 SVYKA	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENHAGEN)	86-111							
PV010 SVYKA	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	92-116	178-203	232-279	218-233	171-605			
PV011 SVYKA	PROTEIN C11	VACCINIA VIRUS (STRAIN COPENHAGEN)	41-49	178-203	232-279	218-233	171-605			
PV012 SVYKA	PROTEIN C12	VACCINIA VIRUS (STRAIN WR)	136-189							
PV013 SVYKA	PROTEIN C13	VARIOLA VIRUS	136-163							
PV014 SVYKA	PROTEIN C14	VACCINIA VIRUS (STRAIN COPENHAGEN)	136-163							
PV015 SVYKA	PROTEIN C15	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3-10	137-182	206-240					
PV016 SVYKA	PROTEIN C16	VACCINIA VIRUS (STRAIN COPENHAGEN)	111-152							
PV017 SVYKA	PROTEIN C17	VACCINIA VIRUS (STRAIN WR)	40-74							
PV018 SVYKA	PROTEIN C18	SHOPE FIBROMA VIRUS (STRAIN KASZA)	58-97							
PV019 SVYKA	PROTEIN C19	VACCINIA VIRUS (STRAIN COPENHAGEN)	72-99							
PV020 SVYKA	PROTEIN C20	VARIOLA VIRUS	299-316							
PV021 SVYKA	PROTEIN C21	EPSTEIN-BARR VIRUS (STRAIN B95.1)	847-874							
PV022 SVYKA	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 STRAIN UGANDA-1102)	136-170	333-382						
PV023 SVYKA	MAJOR CAPSID PROTEIN	HERPES VIRUS SAHARI (STRAIN 11)	169-199							
PV024 SVYKA	MAJOR CAPSID PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXOSIS VIRUS	133-163	196-248						
PV025 SVYKA	MAJOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 2	88-115							
PV026 SVYKA	MAJOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 3	87-114							
PV027 SVYKA	MAJOR CORE PROTEIN	POWELL VIRUS (STRAIN FF-1)	6-33	182-211	331-340					
PV028 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	240-267	333-382						
PV029 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN WR)	240-267							
PV030 SVYKA	MAJOR CORE PROTEIN	VARIOLA VIRUS	240-267							
PV031 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	133-150							
PV032 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN WR)	133-150							
PV033 SVYKA	MAJOR CORE PROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	18-32							
PV034 SVYKA	MAJOR CORE PROTEIN	CARINATHON STORIED RING VIRUS	2-35							
PV035 SVYKA	MAJOR CORE PROTEIN	VARIOLA VIRUS	282-322							
PV036 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-116	417-464						
PV037 SVYKA	MAJOR CORE PROTEIN	VACCINIA VIRUS (STRAIN WR)	89-116	417-464						
PV038 SVYKA	MAJOR CORE PROTEIN	VARIOLA VIRUS	89-116	417-464						
PV039 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	60-87							
PV040 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3A	31-48							
PV041 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3B	168-267							
PV042 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	103-130							
PV043 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	55-59							
PV044 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	35-39							
PV045 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	146-172							
PV046 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	31-48							
PV047 SVYKA	MAJOR CORE PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXOSIS VIRUS	72-113							
PV048 SVYKA	MAJOR CORE PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANKAS)	5-34							
PV049 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5	13-51							
PV050 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 13	137-184	314-361						
PV051 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	81-105	312-342						
PV052 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	312-340							
PV053 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1A	150-186							
PV054 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	150-193							
PV055 SVYKA	MAJOR CORE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	204-311							



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18S1284		All Variants (see BioRxiv.org)		ARCA1	ARCA2	ARCA3	ARCA4	ARCA5	ARCA6	ARCA7	ARCA8	ARCA9	ARCA10	ARCA11	ARCA12	ARCA13	ARCA14	ARCA15	ARCA16	ARCA17	ARCA18	ARCA19	ARCA20	ARCA21	ARCA22	ARCA23	ARCA24	ARCA25	ARCA26	ARCA27	ARCA28	ARCA29	ARCA30	ARCA31	ARCA32	ARCA33	ARCA34	ARCA35	ARCA36	ARCA37	ARCA38	ARCA39	ARCA40	ARCA41	ARCA42	ARCA43	ARCA44	ARCA45	ARCA46	ARCA47	ARCA48	ARCA49	ARCA50	ARCA51	ARCA52	ARCA53	ARCA54	ARCA55	ARCA56	ARCA57	ARCA58	ARCA59	ARCA60	ARCA61	ARCA62	ARCA63	ARCA64	ARCA65	ARCA66	ARCA67	ARCA68	ARCA69	ARCA70	ARCA71	ARCA72	ARCA73	ARCA74	ARCA75	ARCA76	ARCA77	ARCA78	ARCA79	ARCA80	ARCA81	ARCA82	ARCA83	ARCA84	ARCA85	ARCA86	ARCA87	ARCA88	ARCA89	ARCA90	ARCA91	ARCA92	ARCA93	ARCA94	ARCA95	ARCA96	ARCA97	ARCA98	ARCA99	ARCA100	ARCA101	ARCA102	ARCA103	ARCA104	ARCA105	ARCA106	ARCA107	ARCA108	ARCA109	ARCA110	ARCA111	ARCA112	ARCA113	ARCA114	ARCA115	ARCA116	ARCA117	ARCA118	ARCA119	ARCA120	ARCA121	ARCA122	ARCA123	ARCA124	ARCA125	ARCA126	ARCA127	ARCA128	ARCA129	ARCA130	ARCA131	ARCA132	ARCA133	ARCA134	ARCA135	ARCA136	ARCA137	ARCA138	ARCA139	ARCA140	ARCA141	ARCA142	ARCA143	ARCA144	ARCA145	ARCA146	ARCA147	ARCA148	ARCA149	ARCA150	ARCA151	ARCA152	ARCA153	ARCA154	ARCA155	ARCA156	ARCA157	ARCA158	ARCA159	ARCA160	ARCA161	ARCA162	ARCA163	ARCA164	ARCA165	ARCA166	ARCA167	ARCA168	ARCA169	ARCA170	ARCA171	ARCA172	ARCA173	ARCA174	ARCA175	ARCA176	ARCA177	ARCA178	ARCA179	ARCA180	ARCA181	ARCA182	ARCA183	ARCA184	ARCA185	ARCA186	ARCA187	ARCA188	ARCA189	ARCA190	ARCA191	ARCA192	ARCA193	ARCA194	ARCA195	ARCA196	ARCA197	ARCA198	ARCA199	ARCA200	ARCA201	ARCA202	ARCA203	ARCA204	ARCA205	ARCA206	ARCA207	ARCA208	ARCA209	ARCA210	ARCA211	ARCA212	ARCA213	ARCA214	ARCA215	ARCA216	ARCA217	ARCA218	ARCA219	ARCA220	ARCA221	ARCA222	ARCA223	ARCA224	ARCA225	ARCA226	ARCA227	ARCA228	ARCA229	ARCA230	ARCA231	ARCA232	ARCA233	ARCA234	ARCA235	ARCA236	ARCA237	ARCA238	ARCA239	ARCA240	ARCA241	ARCA242	ARCA243	ARCA244	ARCA245	ARCA246	ARCA247	ARCA248	ARCA249	ARCA250	ARCA251	ARCA252	ARCA253	ARCA254	ARCA255	ARCA256	ARCA257	ARCA258	ARCA259	ARCA260	ARCA261	ARCA262	ARCA263	ARCA264	ARCA265	ARCA266	ARCA267	ARCA268	ARCA269	ARCA270	ARCA271	ARCA272	ARCA273	ARCA274	ARCA275	ARCA276	ARCA277	ARCA278	ARCA279	ARCA280	ARCA281	ARCA282	ARCA283	ARCA284	ARCA285	ARCA286	ARCA287	ARCA288	ARCA289	ARCA290	ARCA291	ARCA292	ARCA293	ARCA294	ARCA295	ARCA296	ARCA297	ARCA298	ARCA299	ARCA300	ARCA301	ARCA302	ARCA303	ARCA304	ARCA305	ARCA306	ARCA307	ARCA308	ARCA309	ARCA310	ARCA311	ARCA312	ARCA313	ARCA314	ARCA315	ARCA316	ARCA317	ARCA318	ARCA319	ARCA320	ARCA321	ARCA322	ARCA323	ARCA324	ARCA325	ARCA326	ARCA327	ARCA328	ARCA329	ARCA330	ARCA331	ARCA332	ARCA333	ARCA334	ARCA335	ARCA336	ARCA337	ARCA338	ARCA339	ARCA340	ARCA341	ARCA342	ARCA343	ARCA344	ARCA345	ARCA346	ARCA347	ARCA348	ARCA349	ARCA350	ARCA351	ARCA352	ARCA353	ARCA354	ARCA355	ARCA356	ARCA357	ARCA358	ARCA359	ARCA360	ARCA361	ARCA362	ARCA363	ARCA364	ARCA365	ARCA366	ARCA367	ARCA368	ARCA369	ARCA370	ARCA371	ARCA372	ARCA373	ARCA374	ARCA375	ARCA376	ARCA377	ARCA378	ARCA379	ARCA380	ARCA381	ARCA382	ARCA383	ARCA384	ARCA385	ARCA386	ARCA387	ARCA388	ARCA389	ARCA390	ARCA391	ARCA392	ARCA393	ARCA394	ARCA395	ARCA396	ARCA397	ARCA398	ARCA399	ARCA400	ARCA401	ARCA402	ARCA403	ARCA404	ARCA405	ARCA406	ARCA407	ARCA408	ARCA409	ARCA410	ARCA411	ARCA412	ARCA413	ARCA414	ARCA415	ARCA416	ARCA417	ARCA418	ARCA419	ARCA420	ARCA421	ARCA422	ARCA423	ARCA424	ARCA425	ARCA426	ARCA427	ARCA428	ARCA429	ARCA430	ARCA431	ARCA432	ARCA433	ARCA434	ARCA435	ARCA436	ARCA437	ARCA438	ARCA439	ARCA440	ARCA441	ARCA442	ARCA443	ARCA444	ARCA445	ARCA446	ARCA447	ARCA448	ARCA449	ARCA450	ARCA451	ARCA452	ARCA453	ARCA454	ARCA455	ARCA456	ARCA457	ARCA458	ARCA459	ARCA460	ARCA461	ARCA462	ARCA463	ARCA464	ARCA465	ARCA466	ARCA467	ARCA468	ARCA469	ARCA470	ARCA471	ARCA472	ARCA473	ARCA474	ARCA475	ARCA476	ARCA477	ARCA478	ARCA479	ARCA480	ARCA481	ARCA482	ARCA483	ARCA484	ARCA485	ARCA486	ARCA487	ARCA488	ARCA489	ARCA490	ARCA491	ARCA492	ARCA493	ARCA494	ARCA495	ARCA496	ARCA497	ARCA498	ARCA499	ARCA500	ARCA501	ARCA502	ARCA503	ARCA504	ARCA505	ARCA506	ARCA507	ARCA508	ARCA509	ARCA510	ARCA511	ARCA512	ARCA513	ARCA514	ARCA515	ARCA516	ARCA517	ARCA518	ARCA519	ARCA520	ARCA521	ARCA522	ARCA523	ARCA524	ARCA525	ARCA526	ARCA527	ARCA528	ARCA529	ARCA530	ARCA531	ARCA532	ARCA533	ARCA534	ARCA535	ARCA536	ARCA537	ARCA538	ARCA539	ARCA540	ARCA541	ARCA542	ARCA543	ARCA544	ARCA545	ARCA546	ARCA547	ARCA548	ARCA549	ARCA550	ARCA551	ARCA552	ARCA553	ARCA554	ARCA555	ARCA556	ARCA557	ARCA558	ARCA559	ARCA560	ARCA561	ARCA562	ARCA563	ARCA564	ARCA565	ARCA566	ARCA567	ARCA568	ARCA569	ARCA570	ARCA571	ARCA572	ARCA573	ARCA574	ARCA575	ARCA576	ARCA577	ARCA578	ARCA579	ARCA580	ARCA581	ARCA582	ARCA583	ARCA584	ARCA585	ARCA586	ARCA587	ARCA588	ARCA589	ARCA590	ARCA591	ARCA592	ARCA593	ARCA594	ARCA595	ARCA596	ARCA597	ARCA598	ARCA599	ARCA600	ARCA601	ARCA602	ARCA603	ARCA604	ARCA605	ARCA606	ARCA607	ARCA608	ARCA609	ARCA610	ARCA611	ARCA612	ARCA613	ARCA614	ARCA615	ARCA616	ARCA617	ARCA618	ARCA619	ARCA620	ARCA621	ARCA622	ARCA623	ARCA624	ARCA625	ARCA626	ARCA627	ARCA628	ARCA629	ARCA630	ARCA631	ARCA632	ARCA633	ARCA634	ARCA635	ARCA636	ARCA637	ARCA638	ARCA639	ARCA640	ARCA641	ARCA642	ARCA643	ARCA644	ARCA645	ARCA646	ARCA647	ARCA648	ARCA649	ARCA650	ARCA651	ARCA652	ARCA653	ARCA654	ARCA655	ARCA656	ARCA657	ARCA658	ARCA659	ARCA660	ARCA661	ARCA662	ARCA663	ARCA664	ARCA665	ARCA666	ARCA667	ARCA668	ARCA669	ARCA670	ARCA671	ARCA672	ARCA673	ARCA674	ARCA675	ARCA676	ARCA677	ARCA678	ARCA679	ARCA680	ARCA681	ARCA682	ARCA683	ARCA684	ARCA685	ARCA686	ARCA687	ARCA688	ARCA689	ARCA690	ARCA691	ARCA692	ARCA693	ARCA694	ARCA695	ARCA696	ARCA697	ARCA698	ARCA699	ARCA700	ARCA701	ARCA702	ARCA703	ARCA704	ARCA705	ARCA706	ARCA707	ARCA708	ARCA709	ARCA710	ARCA711	ARCA712	ARCA713	ARCA714	ARCA715	ARCA716	ARCA717	ARCA718	ARCA719	ARCA720	ARCA721	ARCA722	ARCA723	ARCA724	ARCA725	ARCA726	ARCA727	ARCA728	ARCA729	ARCA730	ARCA731	ARCA732	ARCA733	ARCA734	ARCA735	ARCA736	ARCA737	ARCA738	ARCA739	ARCA740	ARCA741	ARCA742	ARCA743	ARCA744	ARCA745	ARCA746	ARCA747	ARCA748	ARCA749	ARCA750	ARCA751	ARCA752	ARCA753	ARCA754	ARCA755	ARCA756	ARCA757	ARCA758	ARCA759	ARCA760	ARCA761	ARCA762	ARCA763	ARCA764	ARCA765	ARCA766	ARCA767	ARCA768	ARCA769	ARCA770	ARCA771	ARCA772	ARCA773	ARCA774	ARCA775	ARCA776	ARCA777	ARCA778	ARCA779	ARCA780	ARCA781	ARCA782	ARCA783	ARCA784	ARCA785	ARCA786	ARCA787	ARCA788	ARCA789	ARCA790	ARCA791	ARCA792	ARCA793	ARCA794	ARCA795	ARCA796	ARCA797	ARCA798	ARCA799	ARCA800	ARCA801	ARCA802	ARCA803	ARCA804	ARCA805	ARCA806	ARCA807	ARCA808	ARCA809	ARCA810	ARCA811	ARCA812	ARCA813	ARCA814	ARCA815	ARCA816	ARCA817	ARCA818	ARCA819	ARCA820	ARCA821	ARCA822	ARCA823	ARCA824	ARCA825	ARCA826	ARCA827	ARCA828	ARCA829	ARCA830	ARCA831	ARCA832	ARCA833	ARCA834	ARCA835	ARCA836	ARCA837	ARCA838	ARCA839	ARCA840	ARCA841	ARCA842	ARCA843	ARCA844	ARCA845	ARCA846	ARCA847	ARCA848	ARCA849	ARCA850	ARCA851	ARCA852	ARCA853	ARCA854	ARCA855	ARCA856	ARCA857	ARCA858	ARCA859	ARCA860	ARCA861	ARCA862	ARCA863	ARCA864	ARCA865	ARCA866	ARCA867	ARCA868	ARCA869	ARCA870	ARCA871	ARCA872	ARCA873	ARCA874	ARCA875	ARCA876	ARCA877	ARCA878	ARCA879	ARCA880	ARCA881	ARCA882	ARCA883	ARCA884	ARCA885	ARCA886	ARCA887	ARCA888	ARCA889	ARCA890	ARCA891	ARCA892	ARCA893	ARCA894	ARCA895	ARCA896	ARCA897	ARCA898	ARCA899	ARCA900	ARCA901	ARCA902	ARCA903	ARCA904	ARCA905	ARCA906	ARCA907	ARCA908	ARCA909	ARCA910	ARCA911	ARCA912	ARCA913	ARCA914	ARCA915	ARCA916	ARCA917	ARCA918	ARCA919	ARCA920	ARCA921	ARCA922	ARCA923	ARCA924	ARCA925	ARCA926	ARCA927	ARCA928	ARCA929	ARCA930	ARCA931	ARCA932	ARCA933	ARCA934	ARCA935	ARCA936	ARCA937	ARCA938	ARCA939	ARCA940	ARCA941	ARCA942	ARCA943	ARCA944	ARCA945	ARCA946	ARCA947	ARCA948	ARCA949	ARCA950	ARCA951	ARCA952	ARCA953	ARCA954	ARCA955	ARCA956	ARCA957	ARCA958	ARCA959	ARCA960	ARCA961	ARCA962	ARCA963	ARCA964	ARCA965	ARCA966	ARCA967	ARCA968	ARCA969	ARCA970	ARCA971	ARCA972	ARCA973	ARCA974	ARCA975	ARCA976	ARCA977	ARCA978	ARCA979	ARCA980	ARCA981	ARCA982	ARCA983	ARCA984	ARCA985	ARCA986	ARCA987	ARCA988	ARCA989	ARCA990	ARCA991	ARCA992	ARCA993	ARCA994	ARCA995	ARCA996	ARCA997	ARCA998	ARCA999	ARCA1000
GENE	18S1284	ALL Variants (see BioRxiv.org)	ARCA1	ARCA2	ARCA3	ARCA4	ARCA5	ARCA6	ARCA7	ARCA8	ARCA9	ARCA10	ARCA11	ARCA12	ARCA13	ARCA14	ARCA15	ARCA16	ARCA17	ARCA18	ARCA19	ARCA20	ARCA21	ARCA22	ARCA23	ARCA24	ARCA25	ARCA26	ARCA27	ARCA28	ARCA29	ARCA30	ARCA31	ARCA32	ARCA33	ARCA34	ARCA35	ARCA36	ARCA37	ARCA38	ARCA39	ARCA40	ARCA41	ARCA42	ARCA43	ARCA44	ARCA45	ARCA46	ARCA47	ARCA48	ARCA49	ARCA50	ARCA51	ARCA52	ARCA53	ARCA54	ARCA55	ARCA56	ARCA57	ARCA58	ARCA59	ARCA60	ARCA61	ARCA62	ARCA63	ARCA64	ARCA65	ARCA66	ARCA67	ARCA68	ARCA69	ARCA70	ARCA71	ARCA72	ARCA73	ARCA74	ARCA75	ARCA76	ARCA77	ARCA78	ARCA79	ARCA80	ARCA81	ARCA82	ARCA83	ARCA84	ARCA85	ARCA86	ARCA87	ARCA88	ARCA89	ARCA90	ARCA91	ARCA92	ARCA93	ARCA94	ARCA95	ARCA96	ARCA97	ARCA98	ARCA99	ARCA100	ARCA101	ARCA102	ARCA103	ARCA104	ARCA105	ARCA106	ARCA107	ARCA108	ARCA109	ARCA110	ARCA111	ARCA112	ARCA113	ARCA114	ARCA115	ARCA116	ARCA117	ARCA118	ARCA119	ARCA120	ARCA121	ARCA122	ARCA123	ARCA124	ARCA125	ARCA126	ARCA127	ARCA128	ARCA129	ARCA130	ARCA131	ARCA132	ARCA133	ARCA134	ARCA135	ARCA136	ARCA137	ARCA138	ARCA139	ARCA140	ARCA141	ARCA142	ARCA143	ARCA144	ARCA145	ARCA146	ARCA147	ARCA148	ARCA149	ARCA150	ARCA151	ARCA152	ARCA153	ARCA154	ARCA155	ARCA156	ARCA157	ARCA158	ARCA159	ARCA160	ARCA161	ARCA162	ARCA163	ARCA164	ARCA165	ARCA166	ARCA167	ARCA168	ARCA169	ARCA170	ARCA171	ARCA172	ARCA173	ARCA174	ARCA175	ARCA176	ARCA177	ARCA178	ARCA179	ARCA180	ARCA181	ARCA182	ARCA183	ARCA184	ARCA185	ARCA186	ARCA187	ARCA188	ARCA189	ARCA190	ARCA191	ARCA192	ARCA193	ARCA194	ARCA195	ARCA196	ARCA197	ARCA198	ARCA199	ARCA200	ARCA201	ARCA202	ARCA203	ARCA204	ARCA205	ARCA206	ARCA207	ARCA208	ARCA209	ARCA210	ARCA211	ARCA212	ARCA213	ARCA214	ARCA215	ARCA216	ARCA217	ARCA218	ARCA219	ARCA220	ARCA221	ARCA222	ARCA223	ARCA224	ARCA225	ARCA226	ARCA227	ARCA228	ARCA229	ARCA230	ARCA231	ARCA232	ARCA233	ARCA234	ARCA235	ARCA236	ARCA237	ARCA238	ARCA239	ARCA240	ARCA241	ARCA242	ARCA243	ARCA244	ARCA245	ARCA246	ARCA247	ARCA248	ARCA249	ARCA250	ARCA251	ARCA252	ARCA25																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												



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126



PC-GENE	1971-1983	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														



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PCGENE	1971714.4	AB Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
ELKABARIE	PROTEIN	VIRUS	11-40	111-145										
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 2 / STRAIN RV-3)	11-40	111-145										
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 2 / STRAIN DS1)	11-40	111-145										
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 2 / STRAIN WA)	111-145											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	RABBIT KOTA VIRUS (SEROTYPE 1 / STRAIN ALABAMA)	111-145											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 KOTA VIRUS (STRAIN SAI1)	111-146											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS	9-46											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MA / SUYAMA)	12-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	9-46											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN HEAVY-LYNH)	9-46											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN KILIAN)	9-46											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	9-46											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	12-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN RW)	9-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN UNABE VACCINE AMP)	12-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	20-63	71-122	127-168	227-239								
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DUNOES)	4-104	110-193										
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN LANG)	4-53	75-104	112-160									
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	316-384											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DUNOES)	318-316											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	90-117											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	90-77											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	CAPULPOVIRUS (STRAIN INS-1)	124-158											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SHOPE FIBROBLAST VIRUS (STRAIN KASZA)	246-237											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	314-390											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	11-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN HERPESVIRUS (TYPE 8 / STRAIN UC-AMPA-1102)	116-201											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	394-421											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN V71)	168-196											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	4-38											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIIBA)	71-65											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-61											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	10-78											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	TORACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	31-47											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	85-112											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	59-86											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	80-107											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	71-111											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	110-153										
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	34-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	34-41											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	91-164											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	118-148											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	24-37											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	231-267											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	133-184											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	132-149											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	56-94											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	81-171	546-573	631-700									
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	13-40											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	FOWL POX VIRUS (ISOLATE HP-431(MUNICH))	74-108	153-179	184-218									
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	FOWL POX VIRUS (ISOLATE HP-431(MUNICH))	63-40											
PV311 ROTHS	MINOR OUTER CAPSID PROTEIN	FOWL POX VIRUS (ISOLATE HP-431(MUNICH))	163-197	214-241										



GENE	1974/1784	AB Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PROTEIN	1974/1784	AB Viruses (no bacteriophages)									
POW1	1974/1784	POW1	11-38								
POW2	1974/1784	POW2	128-167								
POW3	1974/1784	POW3	171-118								
POW4	1974/1784	POW4	171-118								
POW5	1974/1784	POW5	171-118								
POW6	1974/1784	POW6	171-118								
POW7	1974/1784	POW7	171-118								
POW8	1974/1784	POW8	171-118								
POW9	1974/1784	POW9	171-118								
POW10	1974/1784	POW10	171-118								
POW11	1974/1784	POW11	171-118								
POW12	1974/1784	POW12	171-118								
POW13	1974/1784	POW13	171-118								
POW14	1974/1784	POW14	171-118								
POW15	1974/1784	POW15	171-118								
POW16	1974/1784	POW16	171-118								
POW17	1974/1784	POW17	171-118								
POW18	1974/1784	POW18	171-118								
POW19	1974/1784	POW19	171-118								
POW20	1974/1784	POW20	171-118								
POW21	1974/1784	POW21	171-118								
POW22	1974/1784	POW22	171-118								
POW23	1974/1784	POW23	171-118								
POW24	1974/1784	POW24	171-118								
POW25	1974/1784	POW25	171-118								
POW26	1974/1784	POW26	171-118								
POW27	1974/1784	POW27	171-118								
POW28	1974/1784	POW28	171-118								
POW29	1974/1784	POW29	171-118								
POW30	1974/1784	POW30	171-118								
POW31	1974/1784	POW31	171-118								
POW32	1974/1784	POW32	171-118								
POW33	1974/1784	POW33	171-118								
POW34	1974/1784	POW34	171-118								
POW35	1974/1784	POW35	171-118								
POW36	1974/1784	POW36	171-118								
POW37	1974/1784	POW37	171-118								
POW38	1974/1784	POW38	171-118								
POW39	1974/1784	POW39	171-118								
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POW41	1974/1784	POW41	171-118								
POW42	1974/1784	POW42	171-118								
POW43	1974/1784	POW43	171-118								
POW44	1974/1784	POW44	171-118								
POW45	1974/1784	POW45	171-118								
POW46	1974/1784	POW46	171-118								
POW47	1974/1784	POW47	171-118								
POW48	1974/1784	POW48	171-118								
POW49	1974/1784	POW49	171-118								
POW50	1974/1784	POW50	171-118								
POW51	1974/1784	POW51	171-118								
POW52	1974/1784	POW52	171-118								
POW53	1974/1784	POW53	171-118								
POW54	1974/1784	POW54	171-118								
POW55	1974/1784	POW55	171-118								
POW56	1974/1784	POW56	171-118								
POW57	1974/1784	POW57	171-118								
POW58	1974/1784	POW58	171-118								
POW59	1974/1784	POW59	171-118								
POW60	1974/1784	POW60	171-118								
POW61	1974/1784	POW61	171-118								
POW62	1974/1784	POW62	171-118								
POW63	1974/1784	POW63	171-118								
POW64	1974/1784	POW64	171-118								
POW65	1974/1784	POW65	171-118								
POW66	1974/1784	POW66	171-118								
POW67	1974/1784	POW67	171-118								
POW68	1974/1784	POW68	171-118								
POW69	1974/1784	POW69	171-118								
POW70	1974/1784	POW70	171-118								
POW71	1974/1784	POW71	171-118								
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POW134	1974/1784	POW134	171-118								
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POW140	1974/1784	POW140	171-118								
POW141	1974/1784	POW141	171-118								
POW142	1974/1784	POW142	171-118								
POW143	1974/1784	POW143	171-118								
POW144	1974/1784	POW144	171-118								
POW145	1974/1784	POW145	171-118								
POW146	1974/1784	POW146	171-118								
POW147	1974/1784	POW147	171-118								
POW148	1974/1784	POW148	171-118								
POW149	1974/1784	POW149	171-118								
POW150	1974/1784	POW150	171-118								
POW151	1974/1784	POW151	171-118								
POW152	1974/1784	POW1									



TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)



144



145



146



[illegible]



148



149



PCIDAT	1971-1974	1975-1979	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014	2015-2019	2020-2024	2025-2029	2030-2034	2035-2039	2040-2044	2045-2049	2050-2054	2055-2059	2060-2064	2065-2069	2070-2074	2075-2079	2080-2084	2085-2089	2090-2094	2095-2099	2100-2104	2105-2109	2110-2114	2115-2119	2120-2124	2125-2129	2130-2134	2135-2139	2140-2144	2145-2149	2150-2154	2155-2159	2160-2164	2165-2169	2170-2174	2175-2179	2180-2184	2185-2189	2190-2194	2195-2199	2200-2204	2205-2209	2210-2214	2215-2219	2220-2224	2225-2229	2230-2234	2235-2239	2240-2244	2245-2249	2250-2254	2255-2259	2260-2264	2265-2269	2270-2274	2275-2279	2280-2284	2285-2289	2290-2294	2295-2299	2300-2304	2305-2309	2310-2314	2315-2319	2320-2324	2325-2329	2330-2334	2335-2339	2340-2344	2345-2349	2350-2354	2355-2359	2360-2364	2365-2369	2370-2374	2375-2379	2380-2384	2385-2389	2390-2394	2395-2399	2400-2404	2405-2409	2410-2414	2415-2419	2420-2424	2425-2429	2430-2434	2435-2439	2440-2444	2445-2449	2450-2454	2455-2459	2460-2464	2465-2469	2470-2474	2475-2479	2480-2484	2485-2489	2490-2494	2495-2499	2500-2504	2505-2509	2510-2514	2515-2519	2520-2524	2525-2529	2530-2534	2535-2539	2540-2544	2545-2549	2550-2554	2555-2559	2560-2564	2565-2569	2570-2574	2575-2579	2580-2584	2585-2589	2590-2594	2595-2599	2600-2604	2605-2609	2610-2614	2615-2619	2620-2624	2625-2629	2630-2634	2635-2639	2640-2644	2645-2649	2650-2654	2655-2659	2660-2664	2665-2669	2670-2674	2675-2679	2680-2684	2685-2689	2690-2694	2695-2699	2700-2704	2705-2709	2710-2714	2715-2719	2720-2724	2725-2729	2730-2734	2735-2739	2740-2744	2745-2749	2750-2754	2755-2759	2760-2764	2765-2769	2770-2774	2775-2779	2780-2784	2785-2789	2790-2794	2795-2799	2800-2804	2805-2809	2810-2814	2815-2819	2820-2824	2825-2829	2830-2834	2835-2839	2840-2844	2845-2849	2850-2854	2855-2859	2860-2864	2865-2869	2870-2874	2875-2879	2880-2884	2885-2889	2890-2894	2895-2899	2900-2904	2905-2909	2910-2914	2915-2919	2920-2924	2925-2929	2930-2934	2935-2939	2940-2944	2945-2949	2950-2954	2955-2959	2960-2964	2965-2969	2970-2974	2975-2979	2980-2984	2985-2989	2990-2994	2995-2999	3000-3004	3005-3009	3010-3014	3015-3019	3020-3024	3025-3029	3030-3034	3035-3039	3040-3044	3045-3049	3050-3054	3055-3059	3060-3064	3065-3069	3070-3074	3075-3079	3080-3084	3085-3089	3090-3094	3095-3099	3100-3104	3105-3109	3110-3114	3115-3119	3120-3124	3125-3129	3130-3134	3135-3139	3140-3144	3145-3149	3150-3154	3155-3159	3160-3164	3165-3169	3170-3174	3175-3179	3180-3184	3185-3189	3190-3194	3195-3199	3200-3204	3205-3209	3210-3214	3215-3219	3220-3224	3225-3229	3230-3234	3235-3239	3240-3244	3245-3249	3250-3254	3255-3259	3260-3264	3265-3269	3270-3274	3275-3279	3280-3284	3285-3289	3290-3294	3295-3299	3300-3304	3305-3309	3310-3314	3315-3319	3320-3324	3325-3329	3330-3334	3335-3339	3340-3344	3345-3349	3350-3354	3355-3359	3360-3364	3365-3369	3370-3374	3375-3379	3380-3384	3385-3389	3390-3394	3395-3399	3400-3404	3405-3409	3410-3414	3415-3419	3420-3424	3425-3429	3430-3434	3435-3439	3440-3444	3445-3449	3450-3454	3455-3459	3460-3464	3465-3469	3470-3474	3475-3479	3480-3484	3485-3489	3490-3494	3495-3499	3500-3504	3505-3509	3510-3514	3515-3519	3520-3524	3525-3529	3530-3534	3535-3539	3540-3544	3545-3549	3550-3554	3555-3559	3560-3564	3565-3569	3570-3574	3575-3579	3580-3584	3585-3589	3590-3594	3595-3599	3600-3604	3605-3609	3610-3614	3615-3619	3620-3624	3625-3629	3630-3634	3635-3639	3640-3644	3645-3649	3650-3654	3655-3659	3660-3664	3665-3669	3670-3674	3675-3679	3680-3684	3685-3689	3690-3694	3695-3699	3700-3704	3705-3709	3710-3714	3715-3719	3720-3724	3725-3729	3730-3734	3735-3739	3740-3744	3745-3749	3750-3754	3755-3759	3760-3764	3765-3769	3770-3774	3775-3779	3780-3784	3785-3789	3790-3794	3795-3799	3800-3804	3805-3809	3810-3814	3815-3819	3820-3824	3825-3829	3830-3834	3835-3839	3840-3844	3845-3849	3850-3854	3855-3859	3860-3864	3865-3869	3870-3874	3875-3879	3880-3884	3885-3889	3890-3894	3895-3899	3900-3904	3905-3909	3910-3914	3915-3919	3920-3924	3925-3929	3930-3934	3935-3939	3940-3944	3945-3949	3950-3954	3955-3959	3960-3964	3965-3969	3970-3974	3975-3979	3980-3984	3985-3989	3990-3994	3995-3999	4000-4004	4005-4009	4010-4014	4015-4019	4020-4024	4025-4029	4030-4034	4035-4039	4040-4044	4045-4049	4050-4054	4055-4059	4060-4064	4065-4069	4070-4074	4075-4079	4080-4084	4085-4089	4090-4094	4095-4099	4100-4104	4105-4109	4110-4114	4115-4119	4120-4124	4125-4129	4130-4134	4135-4139	4140-4144	4145-4149	4150-4154	4155-4159	4160-4164	4165-4169	4170-4174	4175-4179	4180-4184	4185-4189	4190-4194	4195-4199	4200-4204	4205-4209	4210-4214	4215-4219	4220-4224	4225-4229	4230-4234	4235-4239	4240-4244	4245-4249	4250-4254	4255-4259	4260-4264	4265-4269	4270-4274	4275-4279	4280-4284	4285-4289	4290-4294	4295-4299	4300-4304	4305-4309	4310-4314	4315-4319	4320-4324	4325-4329	4330-4334	4335-4339	4340-4344	4345-4349	4350-4354	4355-4359	4360-4364	4365-4369	4370-4374	4375-4379	4380-4384	4385-4389	4390-4394	4395-4399	4400-4404	4405-4409	4410-4414	4415-4419	4420-4424	4425-4429	4430-4434	4435-4439	4440-4444	4445-4449	4450-4454	4455-4459	4460-4464	4465-4469	4470-4474	4475-4479	4480-4484	4485-4489	4490-4494	4495-4499	4500-4504	4505-4509	4510-4514	4515-4519	4520-4524	4525-4529	4530-4534	4535-4539	4540-4544	4545-4549	4550-4554	4555-4559	4560-4564	4565-4569	4570-4574	4575-4579	4580-4584	4585-4589	4590-4594	4595-4599	4600-4604	4605-4609	4610-4614	4615-4619	4620-4624	4625-4629	4630-4634	4635-4639	4640-4644	4645-4649	4650-4654	4655-4659	4660-4664	4665-4669	4670-4674	4675-4679	4680-4684	4685-4689	4690-4694	4695-4699	4700-4704	4705-4709	4710-4714	4715-4719	4720-4724	4725-4729	4730-4734	4735-4739	4740-4744	4745-4749	4750-4754	4755-4759	4760-4764	4765-4769	4770-4774	4775-4779	4780-4784	4785-4789	4790-4794	4795-4799	4800-4804	4805-4809	4810-4814	4815-4819	4820-4824	4825-4829	4830-4834	4835-4839	4840-4844	4845-4849	4850-4854	4855-4859	4860-4864	4865-4869	4870-4874	4875-4879	4880-4884	4885-4889	4890-4894	4895-4899	4900-4904	4905-4909	4910-4914	4915-4919	4920-4924	4925-4929	4930-4934	4935-4939	4940-4944	4945-4949	4950-4954	4955-4959	4960-4964	4965-4969	4970-4974	4975-4979	4980-4984	4985-4989	4990-4994	4995-4999	5000-5004	5005-5009	5010-5014	5015-5019	5020-5024	5025-5029	5030-5034	5035-5039	5040-5044	5045-5049	5050-5054	5055-5059	5060-5064	5065-5069	5070-5074	5075-5079	5080-5084	5085-5089	5090-5094	5095-5099	5100-5104	5105-5109	5110-5114	5115-5119	5120-5124	5125-5129	5130-5134	5135-5139	5140-5144	5145-5149	5150-5154	5155-5159	5160-5164	5165-5169	5170-5174	5175-5179	5180-5184	5185-5189	5190-5194	5195-5199	5200-5204	5205-5209	5210-5214	5215-5219	5220-5224	5225-5229	5230-5234	5235-5239	5240-5244	5245-5249	5250-5254	5255-5259	5260-5264	5265-5269	5270-5274	5275-5279	5280-5284	5285-5289	5290-5294	5295-5299	5300-5304	5305-5309	5310-5314	5315-5319	5320-5324	5325-5329	5330-5334	5335-5339	5340-5344	5345-5349	5350-5354	5355-5359	5360-5364	5365-5369	5370-5374	5375-5379	5380-5384	5385-5389	5390-5394	5395-5399	5400-5404	5405-5409	5410-5414	5415-5419	5420-5424	5425-5429	5430-5434	5435-5439	5440-5444	5445-5449	5450-5454	5455-5459	5460-5464	5465-5469	5470-5474	5475-5479	5480-5484	5485-5489	5490-5494	5495-5499	5500-5504	5505-5509	5510-5514	5515-5519	5520-5524	5525-5529	5530-5534	5535-5539	5540-5544	5545-5549	5550-5554	5555-5559	5560-5564	5565-5569	5570-5574	5575-5579	5580-5584	5585-5589	5590-5594	5595-5599	5600-5604	5605-5609	5610-5614	5615-5619	5620-5624	5625-5629	5630-5634	5635-5639	5640-5644	5645-5649	5650-5654	5655-5659	5660-5664	5665-5669	5670-5674	5675-5679	5680-5684	5685-5689	5690-5694	5695-5699	5700-5704	5705-5709	5710-5714	5715-5719	5720-5724	5725-5729	5730-5734	5735-5739	5740-5744	5745-5749	5750-5754	5755-5759	5760-5764	5765-5769	5770-5774	5775-5779	5780-5784	5785-5789	5790-5794	5795-5799	5800-5804	5805-5809	5810-5814	5815-5819	5820-5824	5825-5829	5830-5834	5835-5839	5840-5844	5845-5849	5850-5854	5855-5859	5860-5864	5865-5869	5870-5874	5875-5879	5880-5884	5885-5889	5890-5894	5895-5899	5900-5904	5905-5909	5910-5914	5915-5919	5920-5924	5925-5929	5930-5934	5935-5939	5940-5944	5945-5949	5950-5954	5955-5959	5960-5964	5965-5969	5970-5974	5975-5979	5980-5984	5985-5989	5990-5994	5995-5999	6000-6004	6005-6009	6010-6014	6015-6019	6020-6024	6025-6029	6030-6034	6035-6039	6040-6044	6045-6049	6050-6054	6055-6059	6060-6064	6065-6069	6070-6074	6075-6079	6080-6084	6085-6089	6090-6094	6095-6099	6100-6104	6105-6109	6110-6114	6115-6119	6120-6124	6125-6129	6130-6134	6135-6139	6140-6144	6145-6149	6150-6154	6155-6159	6160-6164	6165-6169	6170-6174	6175-6179	6180-6184	6185-6189	6190-6194	6195-6199	6200-6204	6205-6209	6210-6214	6215-6219	6220-6224	6225-6229	6230-6234	6235-6239	6240-6244	6245-6249	6250-6254	6255-6259	6260-6264	6265-6269	6270-6274	6275-6279	6280-6284	6285-6289	6290-6294	6295-6299	6300-6304	6305-6309	6310-6314	6315-6319	6320-6324	6325-6329	6330-6334	6335-6339	6340-6344</
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154



PROTEIN	GENE	191-194	195-198	199-202	203-206	207-210	211-214	215-218	219-222	223-226	227-230	231-234	235-238	239-242	243-246	247-250	251-254	255-258	259-262	263-266	267-270	271-274	275-278	279-282	283-286	287-290	291-294	295-298	299-302	303-306	307-310	311-314	315-318	319-322	323-326	327-330	331-334	335-338	339-342	343-346	347-350	351-354	355-358	359-362	363-366	367-370	371-374	375-378	379-382	383-386	387-390	391-394	395-398	399-402	403-406	407-410	411-414	415-418	419-422	423-426	427-430	431-434	435-438	439-442	443-446	447-450	451-454	455-458	459-462	463-466	467-470	471-474	475-478	479-482	483-486	487-490	491-494	495-498	499-502	503-506	507-510	511-514	515-518	519-522	523-526	527-530	531-534	535-538	539-542	543-546	547-550	551-554	555-558	559-562	563-566	567-570	571-574	575-578	579-582	583-586	587-590	591-594	595-598	599-602	603-606	607-610	611-614	615-618	619-622	623-626	627-630	631-634	635-638	639-642	643-646	647-650	651-654	655-658	659-662	663-666	667-670	671-674	675-678	679-682	683-686	687-690	691-694	695-698	699-702	703-706	707-710	711-714	715-718	719-722	723-726	727-730	731-734	735-738	739-742	743-746	747-750	751-754	755-758	759-762	763-766	767-770	771-774	775-778	779-782	783-786	787-790	791-794	795-798	799-802	803-806	807-810	811-814	815-818	819-822	823-826	827-830	831-834	835-838	839-842	843-846	847-850	851-854	855-858	859-862	863-866	867-870	871-874	875-878	879-882	883-886	887-890	891-894	895-898	899-902	903-906	907-910	911-914	915-918	919-922	923-926	927-930	931-934	935-938	939-942	943-946	947-950	951-954	955-958	959-962	963-966	967-970	971-974	975-978	979-982	983-986	987-990	991-994	995-998	999-1002	1003-1006	1007-1010	1011-1014	1015-1018	1019-1022	1023-1026	1027-1030	1031-1034	1035-1038	1039-1042	1043-1046	1047-1050	1051-1054	1055-1058	1059-1062	1063-1066	1067-1070	1071-1074	1075-1078	1079-1082	1083-1086	1087-1090	1091-1094	1095-1098	1099-1102	1103-1106	1107-1110	1111-1114	1115-1118	1119-1122	1123-1126	1127-1130	1131-1134	1135-1138	1139-1142	1143-1146	1147-1150	1151-1154	1155-1158	1159-1162	1163-1166	1167-1170	1171-1174	1175-1178	1179-1182	1183-1186	1187-1190	1191-1194	1195-1198	1199-1202	1203-1206	1207-1210	1211-1214	1215-1218	1219-1222	1223-1226	1227-1230	1231-1234	1235-1238	1239-1242	1243-1246	1247-1250	1251-1254	1255-1258	1259-1262	1263-1266	1267-1270	1271-1274	1275-1278	1279-1282	1283-1286	1287-1290	1291-1294	1295-1298	1299-1302	1303-1306	1307-1310	1311-1314	1315-1318	1319-1322	1323-1326	1327-1330	1331-1334	1335-1338	1339-1342	1343-1346	1347-1350	1351-1354	1355-1358	1359-1362	1363-1366	1367-1370	1371-1374	1375-1378	1379-1382	
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156



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**TABLE VIII**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**FOR ALL PROCARYOTIC PROTEINS**



GENES	1071/1764	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN		ORGANISM	67-94	340-298	355-393	611-472	744-818	1168-1202		AREA9
120 KD SURFACE-EXPOSED PROTEIN		RICKETTSIA RICKETTSII								AREA10
PIRK RUCI		RICKETTSIA RICKETTSII	67-94	340-298	355-393	611-472	744-818	1168-1202		AREA11
17 KD ANTIGEN PRECURSOR		RICKETTSIA RICKETTSII	241-268	460-487	607-634	734-781	879-936	904-931	1270-1334	1344-1371
190 KD ANTIGEN PRECURSOR (CELL SURFACE)		RICKETTSIA RICKETTSII	2085-2096	2121-2168						1732-1750
PROTEIN		DESULFOCOCCUS MOBILIS	25-33	59-89	120-147					
22 KD DESMO		DESULFOCOCCUS MOBILIS	131-194							
40 KD PROTEIN PRECURSOR		VIBRIO ANGUILLARUM	151-338							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	14-41							
60 KD INNER-MEMBRANE PROTEIN		PROTEUS MIRABILIS	95-122	444-524						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	24-31	218-246						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	205-232							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	205-232							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	450-477							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	146-173							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	151-178							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	176-203							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	85-126	170-204	209-271					
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	127-154							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	198-232							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	48-73							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	41-48	613-640						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	85-112							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	4-31							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	213-247							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	510-551							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	512-550	726-731						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	137-184							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	217-264	316-403						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	1129-1163							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	134-170							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	108-425	654-681	512-556	1003-1032				
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	217-284	870-901	943-977					
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	284-311							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	298-325							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	298-325							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	631-680	779-816						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	271-298							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	43-72							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	90-131	607-724	923-950	990-1017	1109-1199	1382-1414		
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	1557-1584							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	276-307							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	278-305							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	610-681	997-631						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	76-51							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	129-159	163-192						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	19-46							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	3-20	460-493	503-530					
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	31-78	608-633						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	260-312							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	5-32							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	286-316							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	160-194							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	140-176							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	81-115							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	115-142							
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	138-172	338-365						
60 KD INNER-MEMBRANE PROTEIN		ESCHERICHIA COLI	9-36							



GENE	FUNCTION	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PALV1	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PALV2	ALANINE RACEMASE	BACILLUS STEAROTHERMOPHILUS	176-193						
PALV3	ALANINE RACEMASE	BACILLUS SUBTILIS	119-146						
PALV4	ALANINE RACEMASE	BACILLUS SUBTILIS	151-187						
PALV5	ALANINE RACEMASE	BACILLUS SUBTILIS	171-191						
PALV6	ALANINE RACEMASE	STREPTOCOCCUS AUREUS	244-271						
PALV7	ALANINE RACEMASE	STREPTOCOCCUS AUREUS	272-284	446-473					
PALV8	ALANINE RACEMASE	STREPTOCOCCUS AUREUS	72-99						
PALV9	ALANINE RACEMASE	STREPTOCOCCUS AUREUS	181-214						
PALV10	ALANINE RACEMASE	STREPTOCOCCUS AUREUS	111-138	199-226					
PALV11	ALANINE RACEMASE	ESCHERICHIA COLI	231-258						
PALV12	ALANINE RACEMASE	ESCHERICHIA COLI	1-47	72-99					
PALV13	ALANINE RACEMASE	ESCHERICHIA COLI	631-643						
PALV14	ALANINE RACEMASE	ESCHERICHIA COLI	116-137						
PALV15	ALANINE RACEMASE	ESCHERICHIA COLI	281-308						
PALV16	ALANINE RACEMASE	ESCHERICHIA COLI	507-534						
PALV17	ALANINE RACEMASE	ESCHERICHIA COLI	151-178	507-534					
PALV18	ALANINE RACEMASE	ESCHERICHIA COLI	76-104						
PALV19	ALANINE RACEMASE	ESCHERICHIA COLI	280-307						
PALV20	ALANINE RACEMASE	ESCHERICHIA COLI	61-88						
PALV21	ALANINE RACEMASE	ESCHERICHIA COLI	60-87	266-293	1143-1184				
PALV22	ALANINE RACEMASE	ESCHERICHIA COLI	269-296	378-405	459-486				
PALV23	ALANINE RACEMASE	ESCHERICHIA COLI	103-148	480-510					
PALV24	ALANINE RACEMASE	ESCHERICHIA COLI	428-453						
PALV25	ALANINE RACEMASE	ESCHERICHIA COLI	210-237	433-463	613-643				
PALV26	ALANINE RACEMASE	ESCHERICHIA COLI	413-431						
PALV27	ALANINE RACEMASE	ESCHERICHIA COLI	166-193						
PALV28	ALANINE RACEMASE	ESCHERICHIA COLI	102-136						
PALV29	ALANINE RACEMASE	ESCHERICHIA COLI	212-239	437-474					
PALV30	ALANINE RACEMASE	ESCHERICHIA COLI	61-88	441-482					
PALV31	ALANINE RACEMASE	ESCHERICHIA COLI	163-203	381-398					
PALV32	ALANINE RACEMASE	ESCHERICHIA COLI	273-310	546-573	579-608	793-822			
PALV33	ALANINE RACEMASE	ESCHERICHIA COLI	411-448						
PALV34	ALANINE RACEMASE	ESCHERICHIA COLI	173-200	612-642					
PALV35	ALANINE RACEMASE	ESCHERICHIA COLI	212-239						
PALV36	ALANINE RACEMASE	ESCHERICHIA COLI	91-122						
PALV37	ALANINE RACEMASE	ESCHERICHIA COLI	164-196						
PALV38	ALANINE RACEMASE	ESCHERICHIA COLI	91-120	169-203					
PALV39	ALANINE RACEMASE	ESCHERICHIA COLI	51-78						
PALV40	ALANINE RACEMASE	ESCHERICHIA COLI	17-64	583-613					
PALV41	ALANINE RACEMASE	ESCHERICHIA COLI	52-79						
PALV42	ALANINE RACEMASE	ESCHERICHIA COLI	62-89						
PALV43	ALANINE RACEMASE	ESCHERICHIA COLI	478-505						
PALV44	ALANINE RACEMASE	ESCHERICHIA COLI	118-148						
PALV45	ALANINE RACEMASE	ESCHERICHIA COLI	416-450						
PALV46	ALANINE RACEMASE	ESCHERICHIA COLI	133-163	308-335	247-277				
PALV47	ALANINE RACEMASE	ESCHERICHIA COLI	121-148						
PALV48	ALANINE RACEMASE	ESCHERICHIA COLI	276-303	347-374	936-962	987-1014	1210-1234	1381-1408	
PALV49	ALANINE RACEMASE	ESCHERICHIA COLI	60-87	218-245					
PALV50	ALANINE RACEMASE	ESCHERICHIA COLI	102-150	302-329	199-226				
PALV51	ALANINE RACEMASE	ESCHERICHIA COLI	274-301	384-410					
PALV52	ALANINE RACEMASE	ESCHERICHIA COLI	82-109						
PALV53	ALANINE RACEMASE	ESCHERICHIA COLI	84-110						
PALV54	ALANINE RACEMASE	ESCHERICHIA COLI	86-120						
PALV55	ALANINE RACEMASE	ESCHERICHIA COLI	68-95						
PALV56	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV57	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV58	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV59	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV60	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV61	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV62	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV63	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV64	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV65	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV66	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV67	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV68	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV69	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV70	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV71	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV72	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV73	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV74	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV75	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV76	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV77	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV78	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV79	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV80	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV81	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV82	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV83	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV84	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV85	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV86	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV87	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV88	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV89	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV90	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV91	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV92	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV93	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV94	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV95	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV96	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV97	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV98	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV99	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						
PALV100	ALANINE RACEMASE	ESCHERICHIA COLI	48-76						



162



PCGENE	101178.4	Prokaryotic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN									
PATPD SYN1	ATP SYNTHASE DELTA CHAIN	ORGANISUM	100-127							
PATPD SYN2	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	113-147							
PATPD VIBAL	ATP SYNTHASE DELTA CHAIN	VIBRIO ALGINOLYTICUS	110-137							
PATPE BACT1	ATP SYNTHASE EPSILON CHAIN	BACILLUS FIRMIUS	51-80							
PATPE MYCGA	ATP SYNTHASE EPSILON CHAIN	MYCOPLASMA GALLISEPTICUM	99-126							
PATPE PROMO	ATP SYNTHASE EPSILON CHAIN	PROPIONIGENUM MODESTUM	100-127							
PATPE SYN1	ATP SYNTHASE EPSILON CHAIN	SYNECHOCOCCUS SP	100-127							
PATPE ANASP	ATP SYNTHASE B CHAIN	ANABAENA SP	72-106	137-164						
PATPF BACT1	ATP SYNTHASE B CHAIN	BACILLUS FIRMIUS	110-151							
PATPF BACTE	ATP SYNTHASE B CHAIN	BACILLUS MEGATERIUM	55-81	132-170						
PATPF MYCGA	ATP SYNTHASE B CHAIN	MYCOPLASMA GALLISEPTICUM	82-135	130-197						
PATPF SYN1	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	15-49	131-159						
PATPF SYN6	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	12-39	128-155						
PATPF THEP3	ATP SYNTHASE B CHAIN PRECURSOR	THEANOPHILIC BACTERIUM PS.1	50-71							
PATPD ANASP	ATP SYNTHASE GAMMA CHAIN	ANABAENA SP	376-310							
PATPD ECOL1	ATP SYNTHASE GAMMA CHAIN	ESCHERICHIA COLI	233-383							
PATPD MYCGA	ATP SYNTHASE GAMMA CHAIN	MYCOPLASMA GALLISEPTICUM	28-62	92-140						
PATPD RHORU	ATP SYNTHASE GAMMA CHAIN	RHODOSPIRILLUM RUBRUM	270-297							
PATPD SYN1	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	280-302							
PATPD SYN7	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	96-136	280-307						
PATPD ANASP	ATP SYNTHASE B CHAIN	MYCOPLASMA GALLISEPTICUM	133-187							
PATPX BACT1	ATP SYNTHASE BETA CHAIN	BACILLUS FIRMIUS	162-189	336-383						
PATPX RHORU	ATP SYNTHASE B CHAIN	RHODOSPIRILLUM RUBRUM	40-74							
PATPX SYN1	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	13-110	128-155						
PATPX SYN6	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	70-100							
PATP2 BACTE	ATP SYNTHASE PROTEIN I	SYNECHOCOCCUS SP	108-135							
PATP2 SYN1	ATP SYNTHASE PROTEIN I	BACILLUS MEGATERIUM	14-62							
PATP2 SYN7	ATP SYNTHASE PROTEIN I	SYNECHOCOCCUS SP	90-131							
PATV8 PRESO	ATP SYNTHASE PROTEIN I	PREUDONOMAS SYRINGAE	184-211	233-260						
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTERIUM SP	36-53							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTERIUM SP	78-57							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	HALOBACTERIUM HALOBIVUM	145-176							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	HALOBACTERIUM SP	180-214							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	152-186							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	STREPTOCOCCUS AGALACTIAE	92-119	138-204	267-306	314-383	487-524	562-589	1014-1041	
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	VITREOSOLLA SP	119-146							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTERIUM SP	423-450							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	334-361	425-455						
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	122-156							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	468-482							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	31-64							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	6-35							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	1000-1022							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	RHODOBACTER CAPSULATUS	249-276							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	CLOSTRIDIUM PASTERIENSIS	71-99	155-166						
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	PROSTHECOCHLORIS AESTUARII	61-93							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ACETOBACTER XYLINUM	131-158	1051-1082						
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ACETOBACTER XYLINUM	10-37							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ACETOBACTER CALCOACEUS	190-217							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	243-270							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	HAEMOPHILUS INFLUENZAE	31-50							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	HAEMOPHILUS INFLUENZAE	157-184	216-231						
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	HAEMOPHILUS INFLUENZAE	201-239							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	MITROBACTER WINOGRADSKYI	8-33							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	ESCHERICHIA COLI	935-985							
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE	BACILLUS STEAROTHEANOPHILUS	399-433							



164



10117844		Prokaryotic Sequences									
PCGENE	FILENAME	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN	BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR	CLOSTRIDIUM BOTULINUM	114-141	710-773	804-892	798-825	804-831	847-892	1060-1087		
CLOB0	BOTULINUM NEUROTOXIN TYPE D PRECURSOR	CLOSTRIDIUM BOTULINUM	473-500	526-576	727-770	804-831	847-892	1060-1087			
CLOB1	BOTULINUM NEUROTOXIN TYPE E PRECURSOR	CLOSTRIDIUM BOTULINUM	354-391	350-381	704-753	772-811	800-917	992-1019	1115-1149		
CLOB2	BOTULINUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	254-291	350-381	704-753	772-811	800-917	992-1019	1115-1149		
CLOB3	BOTULINUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	669-710	735-772	892-919	1013-1040	1095-1122	1183-1210			
CLOB4	CYTOKROME C320	MICROCYSTIS AERUGINOSA	1-30								
BACT1	PROBABLE CADMIUM-TRANSPORTING ATPASE	BACILLUS FIRMUS	10-37	100-131	165-197	276-306	533-563				
BACT2	PROBABLE CADMIUM-TRANSPORTING ATPASE	STAPHYLOCOCCUS AUREUS	382-399	516-570							
BACT3	TRANSCRIPTIONAL ACTIVATOR CADIC	ESCHERICHIA COLI	14-45	412-443							
BACT4	F1 CAPSULE ANCHORING PROTEIN PRECURSOR	YERSINIA PESTIS	203-240	410-437	530-557	619-646					
BACT5	CAPA PROTEIN	BACILLUS ANTHRACIS	108-128								
BACT6	CAPA PROTEIN	BACILLUS ANTHRACIS	36-70								
BACT7	PROSPHOENOLPYRUVATE CARBOXYLASE	ANACYSTIS NODULANS	248-293								
BACT8	PROSPHOENOLPYRUVATE CARBOXYLASE	ANABAENA SP	98-135	157-184	482-528						
BACT9	PROSPHOENOLPYRUVATE CARBOXYLASE	CORYNEBACTERIUM GLUTAMICUM	13-42								
BACT10	PROSPHOENOLPYRUVATE CARBOXYLASE	ESCHERICHIA COLI	51-63								
BACT11	CARBAMOYL-PHOSPHATE SYNTHETASE	BACILLUS SUBTILIS	374-319								
BACT12	CARBAMOYL-PHOSPHATE SYNTHETASE	BACILLUS SUBTILIS	790-331								
BACT13	CARBAMOYL-PHOSPHATE SYNTHETASE	ESCHERICHIA COLI	454-481								
BACT14	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-24	87-114							
BACT15	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-24	87-114							
BACT16	CHLORAMPHENICOL ACETYLTRANSFERASE	ACTINOTRACHEA CALICOACECTICUS	31-63								
BACT17	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS STEAROTHERMOPHILUS	440-470								
BACT18	PEROXIDASE / CATALASE	ESCHERICHIA COLI	413-480								
BACT19	CATALASE HPI	MICROCOCCUS LUTEUS	515-542	510-607							
BACT20	CATALASE HPI	SALMONELLA TYPHIMURUM	175-202								
BACT21	CATALASE HPI	ESCHERICHIA COLI	84-111								
BACT22	CHLORAMPHENICOL ACETYLTRANSFERASE	CAMPYLOBACTER COLI	88-113								
BACT23	CHLORAMPHENICOL ACETYLTRANSFERASE	CLOSTRIDIUM BUTYRICUM	92-119								
BACT24	CHLORAMPHENICOL ACETYLTRANSFERASE	ESCHERICHIA COLI	92-119								
BACT25	CHLORAMPHENICOL ACETYLTRANSFERASE	PROTEUS MIRABILIS	7-24	87-114							
BACT26	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS INTERMEDIUS	7-24	87-114							
BACT27	CHLORAMPHENICOL ACETYLTRANSFERASE	STREPTOCOCCUS AGALACTIAE	209-236								
BACT28	CHLORAMPHENICOL ACETYLTRANSFERASE	COXIELLA BURNETII	48-75								
BACT29	CARBAMOYLTRANSFERASE Y PRECURSOR	THEMOPHILUS MATTHEWII	48-75								
BACT30	CHLORAMPHENICOL ACETYLTRANSFERASE	ESCHERICHIA COLI	376-401								
BACT31	CHLORAMPHENICOL ACETYLTRANSFERASE	SYNCHOCOCUS SP	376-401								
BACT32	CHLORAMPHENICOL ACETYLTRANSFERASE	SYNCHOCOCUS SP	212-256	331-372	445-486						
BACT33	CHLORAMPHENICOL ACETYLTRANSFERASE	THEMOPHILUS MATTHEWII	305-332								
BACT34	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	419-466	616-643							
BACT35	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	210-231	416-466	615-643						
BACT36	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT37	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT38	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT39	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT40	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT41	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT42	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT43	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT44	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT45	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT46	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT47	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT48	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT49	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT50	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT51	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT52	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT53	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT54	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT55	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT56	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT57	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT58	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT59	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT60	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT61	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT62	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT63	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT64	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT65	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT66	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT67	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT68	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT69	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT70	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT71	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT72	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT73	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT74	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT75	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT76	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT77	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT78	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT79	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT80	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT81	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT82	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT83	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT84	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT85	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT86	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT87	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT88	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT89	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT90	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT91	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT92	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT93	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT94	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT95	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT96	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT97	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT98	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT99	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						
BACT100	CHLORAMPHENICOL ACETYLTRANSFERASE	BACILLUS MACEANS	217-244	422-472	594-641						



166



[illegible]



168



PCGENE	10211784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PC1M0 AC1SP	CYCLOHEXANONE MONOOXYGENASE	ACINETOBACTER SP	419-471								
PC1M7 SYN7	CARBONIC ANHYDRASE	SYNCHOCOCUS SP	110-200								
PC1M8 ECOLI	CYX PROTEIN	ESCHERICHIA COLI	33-80								
PC1M9 ECOLI	CYCLOCHROME O LUBIQUINOL OXIDASE SUBUNIT I	ESCHERICHIA COLI	31-38								
PC1P1 SYN7	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	SYNCHOCOCUS SP	107-141								
PC1P2 ECOLI	SULFATE PERMEASE A PROTEIN	ESCHERICHIA COLI	164-191								
PC1P3 ECOLI	CYS REGULON TRANSCRIPTIONAL ACTIVATOR	ESCHERICHIA COLI	1-30								
PC1P4 ECOLI	CYS REGULON TRANSCRIPTIONAL ACTIVATOR	SALMONELLA TYPHIMURUM	1-10								
PC1P5 ECOLI	SEBINE ACETYL TRANSFERASE	ESCHERICHIA COLI	164-191								
PC1P6 ECOLI	SEBINE ACETYL TRANSFERASE	ESCHERICHIA COLI	164-191								
PC1P7 ECOLI	SIRIQUIN SYNTHASE	ESCHERICHIA COLI	405-432								
PC1P8 ECOLI	SIRIQUIN SYNTHASE	SALMONELLA TYPHIMURUM	64-91								
PC1P9 ECOLI	SULFATE ADENYLYLATE TRANSFERASE SUBUNIT I	ESCHERICHIA COLI	201-228								
PC1P10 ECOLI	SULFATE PERMEASE W PROTEIN	ESCHERICHIA COLI	201-228								
PC1P11 SYN7	SULFATE PERMEASE W PROTEIN	SYNCHOCOCUS SP	311-338								
PC1P12 ECOLI	CATION EFFLUX SYSTEM PROTEIN C2CB	ALCALIGENES EUTROPHUS	241-268								
PC1P13 ECOLI	CATION EFFLUX SYSTEM PROTEIN C2CD	ALCALIGENES EUTROPHUS	135-169								
PC1P14 ECOLI	PENICILLIN-BINDING PROTEIN 3'-PRECUNSOR	BACILLUS SUBTILIS	86-107								
PC1P15 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	137-154								
PC1P16 ECOLI	D-AMINO ACID DEHYDROGENASE	ALTERNONAS HALOPHILUS	322-373								
PC1P17 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	68-91								
PC1P18 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	27-34								
PC1P19 ECOLI	D-AMINO ACID DEHYDROGENASE	BACILLUS SUBTILIS	13-47								
PC1P20 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P21 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P22 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P23 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P24 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P25 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P26 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P27 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P28 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P29 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P30 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P31 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P32 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P33 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P34 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P35 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P36 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P37 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P38 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P39 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P40 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P41 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P42 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P43 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P44 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P45 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P46 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P47 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P48 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P49 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P50 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P51 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P52 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P53 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P54 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P55 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P56 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P57 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P58 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P59 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P60 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P61 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P62 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P63 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P64 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P65 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P66 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P67 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P68 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P69 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P70 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P71 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P72 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P73 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P74 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P75 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P76 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P77 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P78 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P79 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P80 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P81 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P82 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P83 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P84 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P85 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P86 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P87 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P88 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P89 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P90 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P91 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P92 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P93 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P94 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P95 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P96 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P97 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P98 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P99 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								
PC1P100 ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	12-39								



PCGENE	10711714	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
FILE NAME	PROTEIN	ORGANISM	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
P0HGB BACQE	GLUCOSE 1-DEHYDROGENASE B	BACILLUS MEGATERIUM	27-37					
P0HGB ECOLI	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	434-463					
P0HRI ETRVN	KETOLACTYL REDUCTASE I	STREPTOMYCES VIOACEOLIBER	168-195					
P0HLE BACST	LEUCINE DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	192-219					
P0HLO AGRT4	D-LYSINE DEHYDROGENASE	AGROBACTERIUM TURKAFACIENS	117-144					
P0HAI METEX	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	METHYLOBACTERIUM EXTORQUENS	153-187	190-224				
P0HAI METEX	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	METHYLOBACTERIUM ORGANOPHILUM	153-187	190-224				
P0HAI JADE	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	PARACOCCLUS DENTIFICANS	193-222					
P0HAI BACSP	NADH DEHYDROGENASE	BACILLUS SP	284-314					
P0HAI ECOLI	NADH DEHYDROGENASE	ESCHERICHIA COLI	180-214					
P0HAI ECOLI	NADH DEHYDROGENASE	BACILLUS SUBTILIS	71-107	408-433				
P0HOM BACBU	HOMOSELINE DEHYDROGENASE	CORYNEBACTERIUM GLUTAMICUM	105-132					
P0HOM BACBU	HOMOSELINE DEHYDROGENASE	BACILLUS SPHARICUS	212-239					
P0HPI BACSH	PHENYLALANINE DEHYDROGENASE	ESCHERICHIA COLI	482-512					
P0HPI ECOLI	SUCC DEHYDROGENASE FLAVOPROTEIN SUBUNIT	ANABAEANA CYLINDRICA	86-113	130-168				
P0HSS ANACV	SOLUBLE HYDROGENASE 43 KD SUBUNIT	SYNECHOCOCUS SP	123-160					
P0HSS SYNP1	SOLUBLE HYDROGENASE, SMALL SUBUNIT	METHYLOPHILUS MITHILOPHILUS	439-468					
P0HIM METAB	TRIMETHYLAMINE DEHYDROGENASE	ESCHERICHIA COLI	384-411					
P0HIV BACSU	PROBABILE ATP-DEPENDENT HELICASE DING	BACILLUS SUBTILIS	54-83	114-141				
P0HIV BACSU	DIVISION INITIATION PROTEIN	PSEUDOMONAS PUTIDA	91-120	374-276				
P0HDS PREPU	DIHYDROLIPOAMIDE DEHYDROGENASE	ALZOTOBACTER VINELANDII	18-45					
P0HDS AZOV1	LIPOLAMIDE DEHYDROGENASE COMP (E1)	BACILLUS STEAROTHERMOPHILUS	82-109					
P0HDS BACST	LIPOLAMIDE DEHYDROGENASE COMP (E2)	BACILLUS SUBTILIS	108-135					
P0HDS BACSU	LIPOLAMIDE DEHYDROGENASE COMP (E3)	ESCHERICHIA COLI	124-151	333-375				
P0HDS ECOLI	DIHYDROLIPOAMIDE DEHYDROGENASE	PSEUDOMONAS FLUORESCENS	61-90	548-581				
P0HDS PREPU	DIHYDROLIPOAMIDE DEHYDROGENASE	PSEUDOMONAS PUTIDA	438-463					
P0HAI BACSU	PHENOL HYDROXYLASE P1 PROTEIN	BACILLUS SUBTILIS	116-140					
P0HAI BACSU	DNAA PROTEIN	BACILLUS SUBTILIS	182-216	248-275	341-387	436-463		
P0HAI BACSU	DNAA PROTEIN	BORRELLIA BURGDORFERI	71-100	111-118	353-360			
P0HAI BUCAP	DNAA PROTEIN	BORRELLIA AFRIDICOLA	164-400					
P0HAI ECOLI	DNAA PROTEIN	ESCHERICHIA COLI	181-415					
P0HAI MYCCA	DNAA PROTEIN	MICROCOCCUS LUTEUS	8-56	75-112	274-310	350-389		
P0HAI BACSU	DNAA PROTEIN	MYCOPLASMA CAPRICOLUM	163-399					
P0HAI BACSU	DNAA PROTEIN	PROTEUS MIRABILIS	398-419					
P0HAI BACSU	DNAA PROTEIN	PSEUDOMONAS PUTIDA	43-72	36-110	165-180			
P0HAI SPICI	DNAA PROTEIN	SPYROPLASMA CITRI	312-353					
P0HAI CHLTR	DNAB-LIKE PROTEIN	CHLAMYDIA TRACHOMATIS	82-109					
P0HAI ECOLI	DNAB PROTEIN	ESCHERICHIA COLI	82-109					
P0HAI ECOLI	DNAB PROTEIN	SALMONELLA TYPHIMURUM	146-190					
P0HAI ECOLI	DNAB PROTEIN	ESCHERICHIA COLI	483-524	548-581				
P0HAI BACME	DNAB PROTEIN	BORRELLIA BURGDORFERI	312-594					
P0HAI BACBU	DNAB PROTEIN	BORRELLIA BURGDORFERI	248-275	312-348				
P0HAI BACBU	DNAB PROTEIN	BRUCELLA OVIS	561-588					
P0HAI BACBU	DNAB PROTEIN	CALOBACTER CRESCENTUS	499-528					
P0HAI CALCA	DNAB PROTEIN	CLOSTRIDIUM ACETOBIUTYLICUM	494-537					
P0HAI CLOAB	DNAB PROTEIN	CLOSTRIDIUM PEURKINGENS	527-539					
P0HAI CLOPE	DNAB PROTEIN	METHANOCALCIVUS MAZEI	502-539					
P0HAI METMA	DNAB PROTEIN	MYCOBACTERIUM TUBERCULOSIS	43-72	533-572				
P0HAI MYCTU	DNAB PROTEIN	STREPTOMYCES COELICOLOR	114-141					
P0HAI STROO	REGULATORY PROTEIN DNAB	ESCHERICHIA COLI	518-512					
P0HAI ZYMMO	DNAA LIASE	ZYTHOMONAS MOBILIS	74-51					
P0HRI STRPE	TRANSDUCTION PROTEIN DNAB	STREPTOMYCES PEUCETIUS	104-172					
P0HCK SULSO	PROBABLE SIGNAL RECOGNITION PARTICLE PROTEIN	SUBLOBOLUS SOLFAFARICUS	58-85	417-444	1382-1416			
P0HAI BACSU	DNAA POLYMERASE III, ALPHA CHAIN	BACILLUS SUBTILIS	71-104					
P0HAI ECOLI	DNAA POLYMERASE III, ALPHA CHAIN	ESCHERICHIA COLI	230-251					
P0HAI SAGER	DNAA POLYMERASE III, ALPHA CHAIN	SACCHAROPOLYSPOA ERYTHRAEA						



PGCENE	10117844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PE01	PROTEIN	ORGANISM	71-104								
PE02	DNA POLYMERASE III, ALPHA CHAIN	SALMONELLA TYPHIMURUM	313-319								
PE03	DNA POLYMERASE III, BETA CHAIN	BACILLUS SUBTILIS	266-311								
PE04	DNA POLYMERASE III, BETA CHAIN	BORRELIA BURGDORFERI	31-42	308-339							
PE05	DNA POLYMERASE III, BETA CHAIN	BACILLUS ADIPOCOLA	191-218								
PE06	DNA POLYMERASE III, BETA CHAIN	MICROCOCCUS LUTEUS	16-30								
PE07	DNA POLYMERASE III, BETA CHAIN	MYCOPLASMA CAPRICOLUM	10-40								
PE08	DNA POLYMERASE III, BETA CHAIN	PSUDOMONAS CITRUS	78-112	199-177	273-310						
PE09	DNA POLYMERASE III, BETA CHAIN	BACILLUS SUBTILIS	331-372								
PE10	DNA POLYMERASE III, SUBUNIT 2	ESCHERICHIA COLI	891-941								
PE11	DNA POLYMERASE III, SUBUNIT 3	ESCHERICHIA COLI	401-448								
PE12	DNA POLYMERASE III, SUBUNIT 4	STREPTOCOCCUS PNEUMONIAE	79-120								
PE13	DNA POLYMERASE I	BACILLUS CALDOSTENAX	208-235								
PE14	DNA POLYMERASE I	STREPTOCOCCUS PNEUMONIAE	198-235	398-425	371-508	645-672					
PE15	DNA POLYMERASE I	THEMUS AQUATICUS	196-221	602-639							
PE16	DNA POLYMERASE II	ESCHERICHIA COLI	592-628								
PE17	DNA POLYMERASE II	STREPTOCOCCUS FURIOSUS	346-396								
PE18	DNA POLYMERASE II	STREPTOCOCCUS FURIOSUS	746-773								
PE19	DNA POLYMERASE II	SULFOLOBUS SOLFATARICUS	379-406	436-463	621-659	747-774					
PE20	DNA POLYMERASE II	THEMUS AQUATICUS	312-370	531-589	892-926	1004-1031	1153-1194				
PE21	DNA POLYMERASE II	LACTOCOCCUS LACTIS	716-733								
PE22	DNA POLYMERASE II	LACTOCOCCUS LACTIS	716-733								
PE23	DNA POLYMERASE II	ESCHERICHIA COLI	4-45								
PE24	DNA POLYMERASE II	STREPTOCOCCUS EQUISIMILIS	31-60	291-318							
PE25	DNA POLYMERASE II	STREPTOCOCCUS PEUCETUS	186-213								
PE26	DNA POLYMERASE II	STAPHYLOCOCCUS AUREUS	62-89								
PE27	DNA POLYMERASE II	BACILLUS CIRCULANS	134-161	305-339	424-451						
PE28	DNA POLYMERASE II	ESCHERICHIA COLI	66-100	158-185	323-352	691-725	102-836	811-903			
PE29	DNA POLYMERASE II	ESCHERICHIA COLI	131-178								
PE30	DNA POLYMERASE II	STAPHYLOCOCCUS AUREUS	68-98								
PE31	DNA POLYMERASE II	STAPHYLOCOCCUS AUREUS	232-249								
PE32	DNA POLYMERASE II	ESCHERICHIA COLI	26-47								
PE33	DNA POLYMERASE II	STAPHYLOCOCCUS AUREUS	12-39								
PE34	DNA POLYMERASE II	STAPHYLOCOCCUS AUREUS	32-79	119-146							
PE35	DNA POLYMERASE II	DESULFOCOCCUS NIGRILIS	427-461								
PE36	DNA POLYMERASE II	HALOBACTERIUM HALOBUTUM	186-213								
PE37	DNA POLYMERASE II	METHANOCOCCUS VANNIELII	409-436								
PE38	DNA POLYMERASE II	SULFOLOBUS ACIDICOLARIS	16-43	145-180							
PE39	DNA POLYMERASE II	THEMUS AQUATICUS	13-40	49-76	220-247						
PE40	DNA POLYMERASE II	ANACYSTIS NIDULANS	332-359								
PE41	DNA POLYMERASE II	ESCHERICHIA COLI	214-261								
PE42	DNA POLYMERASE II	MYCOBACTERIUM LEPRAE	211-239	320-357							
PE43	DNA POLYMERASE II	SALMONELLA TYPHIMURUM	314-361								
PE44	DNA POLYMERASE II	SPRULINA PLATENSIS	314-374	481-511							
PE45	DNA POLYMERASE II	SYNECHOCYSTIS SP	14-21								
PE46	DNA POLYMERASE II	STREPTOMYCES RABDOSSINUS	231-238								
PE47	DNA POLYMERASE II	STREPTOMYCES RABDOSSINUS	231-238								
PE48	DNA POLYMERASE II	STREPTOMYCES RABDOSSINUS	231-238								
PE49	DNA POLYMERASE II	ESCHERICHIA COLI	101-123								
PE50	DNA POLYMERASE II	SPRULINA CITRUS	27-34	134-161							
PE51	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE52	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE53	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE54	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE55	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE56	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE57	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE58	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE59	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE60	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE61	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE62	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE63	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE64	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE65	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE66	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE67	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE68	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE69	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE70	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE71	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE72	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE73	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE74	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE75	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE76	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE77	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE78	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE79	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE80	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE81	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE82	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE83	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE84	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE85	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE86	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE87	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE88	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE89	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE90	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE91	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE92	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE93	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE94	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE95	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE96	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE97	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE98	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE99	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							
PE00	DNA POLYMERASE II	BACILLUS SUBTILIS	11-45	239-256							



[illegible]



PCGENE	10117184	Fraser, J. K. S. et al.	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
PCGENE	10117184	Fraser, J. K. S. et al.	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												



174



PCGENE	10717614	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN										
PRDA ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ORGANISMA	399-422								
PRDA ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	435	487-514							
PRDA WOLU	GLUTING MOTILITY REGULATORY PROTEIN	WOLINELLA SUCCINOGENES	13-42	478-505							
PRDA WOLU	GLUTING MOTILITY REGULATORY PROTEIN	MYXOCOCCUS XANTHUS	161-190								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	CLONOSTRIDIUM THERMAOACETUM	6-43								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	METHANOBACTERIUM THERMAOACETUM	76-110								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	301-338	375-418							
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	6-31								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	61-90								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	151-188								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	218-205								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	210-260								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	7-45								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	290-317								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS STEAROTHERMOPHILUS	414-445								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	95-130								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	YERSINIA PESTIS	303-329								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	37-114								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ANABAEANA VARIABILIS	162-189								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ANABAEANA VARIABILIS	216-224								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	46-76	227-271							
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS MEGATERIUM	49-76								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	239-286								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	MYCOCCUS WOESSEI	290-328								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	THELMOGLOA MARITIMA	101-143	241-269							
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS STEAROTHERMOPHILUS	301-328								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	163-193								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ZYMONOMAS MOBILIS	178-203								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	PSEUDOMONAS FLUORESCENS	86-113								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	SALMONELLA TYPHIMURUM	124-158	219-269							
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	HAEMOPHILUS INFLUENZAE	304-338								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	LACTOBACILLUS HELVETICUS	51-91								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	SALMONELLA TYPHIMURUM	181-209								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	HAEMOPHILUS INFLUENZAE	351-278								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	PSEUDOMONAS FLUORESCENS	78-105								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	197-227	246-273							
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	PHOTOBACTERIUM LEIGNATHI	10-37								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	216-246								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	60-94								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	34-51								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	46-83	182-216	350-384						
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	293-323								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	13-40								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	6-33								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	STAPHYLOCOCCUS HAEMOLYTICUS	6-33								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	STAPHYLOCOCCUS HAEMOLYTICUS	198-223								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	531-568								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	539-566								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	PSEUDOMONAS PUTIDA	14-41								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS SUBTILIS	25-52								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	PSEUDOMONAS PUTIDA	128-122								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	SYNCHOCYSTIS SP	20-79								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	BACILLUS STEAROTHERMOPHILUS	114-141								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	114-141								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	SALMONELLA TYPHIMURUM	209-243								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	ESCHERICHIA COLI	18-45								
PTTHS CLOTH	FOSMATE-TRIPANTHROLYLATE LIGASE	METHANOCOCCUS THERMOTROPHICUS	18-45								



176



FCGENE	1011718.4	Prokaryotic Sequences	ABLA3	ABLA2	ABLA1	ABLA2	ABLA1	ABLA3	ABLA2
GLG1	PROTEIN	ORGANISM	230-317						
GLG2	PROTEIN	XANTHOMONAS CAMPESTRIS	230-317						
GLG3	PROTEIN	GLYCOSYL TRANSFERASE-1	18-59						
GLG4	PROTEIN	GLYCOSYL TRANSFERASE-2	27-41						
GLG5	PROTEIN	GLYCOSYL TRANSFERASE-3	27-41						
GLG6	PROTEIN	GLYCOSYL TRANSFERASE-4	27-41						
GLG7	PROTEIN	GLYCOSYL TRANSFERASE-5	27-41						
GLG8	PROTEIN	GLYCOSYL TRANSFERASE-6	27-41						
GLG9	PROTEIN	GLYCOSYL TRANSFERASE-7	27-41						
GLG10	PROTEIN	GLYCOSYL TRANSFERASE-8	27-41						
GLG11	PROTEIN	GLYCOSYL TRANSFERASE-9	27-41						
GLG12	PROTEIN	GLYCOSYL TRANSFERASE-10	27-41						
GLG13	PROTEIN	GLYCOSYL TRANSFERASE-11	27-41						
GLG14	PROTEIN	GLYCOSYL TRANSFERASE-12	27-41						
GLG15	PROTEIN	GLYCOSYL TRANSFERASE-13	27-41						
GLG16	PROTEIN	GLYCOSYL TRANSFERASE-14	27-41						
GLG17	PROTEIN	GLYCOSYL TRANSFERASE-15	27-41						
GLG18	PROTEIN	GLYCOSYL TRANSFERASE-16	27-41						
GLG19	PROTEIN	GLYCOSYL TRANSFERASE-17	27-41						
GLG20	PROTEIN	GLYCOSYL TRANSFERASE-18	27-41						
GLG21	PROTEIN	GLYCOSYL TRANSFERASE-19	27-41						
GLG22	PROTEIN	GLYCOSYL TRANSFERASE-20	27-41						
GLG23	PROTEIN	GLYCOSYL TRANSFERASE-21	27-41						
GLG24	PROTEIN	GLYCOSYL TRANSFERASE-22	27-41						
GLG25	PROTEIN	GLYCOSYL TRANSFERASE-23	27-41						
GLG26	PROTEIN	GLYCOSYL TRANSFERASE-24	27-41						
GLG27	PROTEIN	GLYCOSYL TRANSFERASE-25	27-41						
GLG28	PROTEIN	GLYCOSYL TRANSFERASE-26	27-41						
GLG29	PROTEIN	GLYCOSYL TRANSFERASE-27	27-41						
GLG30	PROTEIN	GLYCOSYL TRANSFERASE-28	27-41						
GLG31	PROTEIN	GLYCOSYL TRANSFERASE-29	27-41						
GLG32	PROTEIN	GLYCOSYL TRANSFERASE-30	27-41						
GLG33	PROTEIN	GLYCOSYL TRANSFERASE-31	27-41						
GLG34	PROTEIN	GLYCOSYL TRANSFERASE-32	27-41						
GLG35	PROTEIN	GLYCOSYL TRANSFERASE-33	27-41						
GLG36	PROTEIN	GLYCOSYL TRANSFERASE-34	27-41						
GLG37	PROTEIN	GLYCOSYL TRANSFERASE-35	27-41						
GLG38	PROTEIN	GLYCOSYL TRANSFERASE-36	27-41						
GLG39	PROTEIN	GLYCOSYL TRANSFERASE-37	27-41						
GLG40	PROTEIN	GLYCOSYL TRANSFERASE-38	27-41						
GLG41	PROTEIN	GLYCOSYL TRANSFERASE-39	27-41						
GLG42	PROTEIN	GLYCOSYL TRANSFERASE-40	27-41						
GLG43	PROTEIN	GLYCOSYL TRANSFERASE-41	27-41						
GLG44	PROTEIN	GLYCOSYL TRANSFERASE-42	27-41						
GLG45	PROTEIN	GLYCOSYL TRANSFERASE-43	27-41						
GLG46	PROTEIN	GLYCOSYL TRANSFERASE-44	27-41						
GLG47	PROTEIN	GLYCOSYL TRANSFERASE-45	27-41						
GLG48	PROTEIN	GLYCOSYL TRANSFERASE-46	27-41						
GLG49	PROTEIN	GLYCOSYL TRANSFERASE-47	27-41						
GLG50	PROTEIN	GLYCOSYL TRANSFERASE-48	27-41						
GLG51	PROTEIN	GLYCOSYL TRANSFERASE-49	27-41						
GLG52	PROTEIN	GLYCOSYL TRANSFERASE-50	27-41						
GLG53	PROTEIN	GLYCOSYL TRANSFERASE-51	27-41						
GLG54	PROTEIN	GLYCOSYL TRANSFERASE-52	27-41						
GLG55	PROTEIN	GLYCOSYL TRANSFERASE-53	27-41						
GLG56	PROTEIN	GLYCOSYL TRANSFERASE-54	27-41						
GLG57	PROTEIN	GLYCOSYL TRANSFERASE-55	27-41						
GLG58	PROTEIN	GLYCOSYL TRANSFERASE-56	27-41						
GLG59	PROTEIN	GLYCOSYL TRANSFERASE-57	27-41						
GLG60	PROTEIN	GLYCOSYL TRANSFERASE-58	27-41						
GLG61	PROTEIN	GLYCOSYL TRANSFERASE-59	27-41						
GLG62	PROTEIN	GLYCOSYL TRANSFERASE-60	27-41						
GLG63	PROTEIN	GLYCOSYL TRANSFERASE-61	27-41						
GLG64	PROTEIN	GLYCOSYL TRANSFERASE-62	27-41						
GLG65	PROTEIN	GLYCOSYL TRANSFERASE-63	27-41						
GLG66	PROTEIN	GLYCOSYL TRANSFERASE-64	27-41						
GLG67	PROTEIN	GLYCOSYL TRANSFERASE-65	27-41						
GLG68	PROTEIN	GLYCOSYL TRANSFERASE-66	27-41						
GLG69	PROTEIN	GLYCOSYL TRANSFERASE-67	27-41						
GLG70	PROTEIN	GLYCOSYL TRANSFERASE-68	27-41						
GLG71	PROTEIN	GLYCOSYL TRANSFERASE-69	27-41						
GLG72	PROTEIN	GLYCOSYL TRANSFERASE-70	27-41						
GLG73	PROTEIN	GLYCOSYL TRANSFERASE-71	27-41						
GLG74	PROTEIN	GLYCOSYL TRANSFERASE-72	27-41						
GLG75	PROTEIN	GLYCOSYL TRANSFERASE-73	27-41						
GLG76	PROTEIN	GLYCOSYL TRANSFERASE-74	27-41						
GLG77	PROTEIN	GLYCOSYL TRANSFERASE-75	27-41						
GLG78	PROTEIN	GLYCOSYL TRANSFERASE-76	27-41						
GLG79	PROTEIN	GLYCOSYL TRANSFERASE-77	27-41						
GLG80	PROTEIN	GLYCOSYL TRANSFERASE-78	27-41						
GLG81	PROTEIN	GLYCOSYL TRANSFERASE-79	27-41						
GLG82	PROTEIN	GLYCOSYL TRANSFERASE-80	27-41						
GLG83	PROTEIN	GLYCOSYL TRANSFERASE-81	27-41						
GLG84	PROTEIN	GLYCOSYL TRANSFERASE-82	27-41						
GLG85	PROTEIN	GLYCOSYL TRANSFERASE-83	27-41						
GLG86	PROTEIN	GLYCOSYL TRANSFERASE-84	27-41						
GLG87	PROTEIN	GLYCOSYL TRANSFERASE-85	27-41						
GLG88	PROTEIN	GLYCOSYL TRANSFERASE-86	27-41						
GLG89	PROTEIN	GLYCOSYL TRANSFERASE-87	27-41						
GLG90	PROTEIN	GLYCOSYL TRANSFERASE-88	27-41						
GLG91	PROTEIN	GLYCOSYL TRANSFERASE-89	27-41						
GLG92	PROTEIN	GLYCOSYL TRANSFERASE-90	27-41						
GLG93	PROTEIN	GLYCOSYL TRANSFERASE-91	27-41						
GLG94	PROTEIN	GLYCOSYL TRANSFERASE-92	27-41						
GLG95	PROTEIN	GLYCOSYL TRANSFERASE-93	27-41						
GLG96	PROTEIN	GLYCOSYL TRANSFERASE-94	27-41						
GLG97	PROTEIN	GLYCOSYL TRANSFERASE-95	27-41						
GLG98	PROTEIN	GLYCOSYL TRANSFERASE-96	27-41						
GLG99	PROTEIN	GLYCOSYL TRANSFERASE-97	27-41						
GLG100	PROTEIN	GLYCOSYL TRANSFERASE-98	27-41						
GLG101	PROTEIN	GLYCOSYL TRANSFERASE-99	27-41						
GLG102	PROTEIN	GLYCOSYL TRANSFERASE-100	27-41						
GLG103	PROTEIN	GLYCOSYL TRANSFERASE-101	27-41						
GLG104	PROTEIN	GLYCOSYL TRANSFERASE-102	27-41						
GLG105	PROTEIN	GLYCOSYL TRANSFERASE-103	27-41						
GLG106	PROTEIN	GLYCOSYL TRANSFERASE-104	27-41						
GLG107	PROTEIN	GLYCOSYL TRANSFERASE-105	27-41						
GLG108	PROTEIN	GLYCOSYL TRANSFERASE-106	27-41						
GLG109	PROTEIN	GLYCOSYL TRANSFERASE-107	27-41						
GLG110	PROTEIN	GLYCOSYL TRANSFERASE-108	27-41						
GLG111	PROTEIN	GLYCOSYL TRANSFERASE-109	27-41						
GLG112	PROTEIN	GLYCOSYL TRANSFERASE-110	27-41						
GLG113	PROTEIN	GLYCOSYL TRANSFERASE-111	27-41						
GLG114	PROTEIN	GLYCOSYL TRANSFERASE-112	27-41						
GLG115	PROTEIN	GLYCOSYL TRANSFERASE-113	27-41						
GLG116	PROTEIN	GLYCOSYL TRANSFERASE-114	27-41						
GLG117	PROTEIN	GLYCOSYL TRANSFERASE-115	27-41						
GLG118	PROTEIN	GLYCOSYL TRANSFERASE-116	27-41						
GLG119	PROTEIN	GLYCOSYL TRANSFERASE-117	27-41						
GLG120	PROTEIN	GLYCOSYL TRANSFERASE-118	27-41						
GLG121	PROTEIN	GLYCOSYL TRANSFERASE-119	27-41						
GLG122	PROTEIN	GLYCOSYL TRANSFERASE-120	27-41						
GLG123	PROTEIN	GLYCOSYL TRANSFERASE-121	27-41						
GLG124	PROTEIN	GLYCOSYL TRANSFERASE-122	27-41						
GLG125	PROTEIN	GLYCOSYL TRANSFERASE-123	27-41						
GLG126	PROTEIN	GLYCOSYL TRANSFERASE-124	27-41						
GLG127	PROTEIN	GLYCOSYL TRANSFERASE-125	27-41						
GLG128	PROTEIN	GLYCOSYL TRANSFERASE-126	27-41						
GLG129	PROTEIN	GLYCOSYL TRANSFERASE-127	27-41						
GLG130	PROTEIN	GLYCOSYL TRANSFERASE-128	27-41						
GLG131	PROTEIN	GLYCOSYL TRANSFERASE-129	27-41						
GLG132	PROTEIN	GLYCOSYL TRANSFERASE-130	27-41						
GLG133	PROTEIN	GLYCOSYL TRANSFERASE-131	27-41						
GLG134	PROTEIN	GLYCOSYL TRANSFERASE-132	27-41						
GLG135	PROTEIN	GLYCOSYL TRANSFERASE-133	27-41						
GLG136	PROTEIN	GLYCOSYL TRANSFERASE-134	27-41						
GLG137	PROTEIN	GLYCOSYL TRANSFERASE-135	27-41						
GLG138	PROTEIN	GLYCOSYL TRANSFERASE-136	27-41						
GLG139	PROTEIN	GLYCOSYL TRANSFERASE-137	27-41						
GLG140	PROTEIN	GLYCOSYL TRANSFERASE-138	27-41						
GLG141	PROTEIN	GLYCOSYL TRANSFERASE-139	27-41						
GLG142	PROTEIN	GLYCOSYL TRANSFERASE-140	27-41						
GLG143	PROTEIN	GLYCOSYL TRANSFERASE-141	27-41						
GLG144	PROTEIN	GLYCOSYL TRANSFERASE-142	27-41						
GLG145	PROTEIN	GLYCOSYL TRANSFERASE-143	27-41						
GLG146	PROTEIN	GLYCOSYL TRANSFERASE-144	27-41						
GLG147	PROTEIN	GLYCOSYL TRANSFERASE-145	27-41						
GLG148	PROTEIN	GLYCOSYL TRANSFERASE-146	27-41						
GLG149	PROTEIN	GLYCOSYL TRANSFERASE-147	27-41						
GLG150	PROTEIN	GLYCOSYL TRANSFERASE-148	27-41						
GLG151	PROTEIN	GLYCOSYL TRANSFERASE-149	27-41						
GLG152	PROTEIN	GLYCOSYL TRANSFERASE-150	27-41						
GLG153	PROTEIN	GLYCOSYL TRANSFERASE-151	27-41						
GLG154	PROTEIN	GLYCOSYL TRANSFERASE-152	27-41						
GLG155	PROTEIN	GLYCOSYL TRANSFERASE-153	27-41						
GLG156	PROTEIN	GLYCOSYL TRANSFERASE-154	27-41						
GLG157	PROTEIN	GLYCOSYL TRANSFERASE-155	27-41						
GLG158	PROTEIN	GLYCOSYL TRANSFERASE-156	27-41						
GLG159	PROTEIN	GLYCOSYL TRANSFERASE-157	27-41						
GLG160	PROTEIN	GLYCOSYL TRANSFERASE-158	27-41						
GLG161	PROTEIN	GLYCOSYL TRANSFERASE-159	27-41						
GLG162	PROTEIN	GLYCOSYL TRANSFERASE-160	27-41						
GLG163	PROTEIN	GLYCOSYL TRANSFERASE-161	27-41						
GLG164	PROTEIN	GLYCOSYL TRANSFERASE-162	27-41						
GLG165	PROTEIN	GLYCOSYL TRANSFERASE-163	27-41						
GLG166	PROTEIN	GLYCOSYL TRANSFERASE-164	27-41						
GLG167	PROTEIN	GLYCOSYL TRANSFERASE-165	27-41						
GLG168	PROTEIN	GLYCOSYL TRANSFERASE-166	27-41						
GLG169	PROTEIN	GLYCOSYL TRANSFERASE-167	27-41						
GLG170	PROTEIN	GLYCOSYL TRANSFERASE-168	27-41						
GLG171	PROTEIN	GLYCOSYL TRANSFERASE-169	27-41						
GLG172	PROTEIN	GLYCOSYL TRANSFERASE-170	27-41						
GLG173	PROTEIN	GLYCOSYL TRANSFERASE-171	27-41						
GLG174	PROTEIN	GLYCOSYL TRANSFERASE-172	27-41						







179



180



[illegible]



182



PGCENE	1074.17814	Proteolytic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN	ORGANISM										
ALPHA CHAIN	KRYPTONHARON ALFREDI		190-217								AREA2
BETA CHAIN	PHOTODACTERIUM PHOSPHOREUM		118-217	237-291							AREA3
BETA CHAIN	VIBRIO HAARVEI		371-400								AREA4
BETA CHAIN	PHOTODACTERIUM LEIOGNATHI		44-81								AREA5
BETA CHAIN	PHOTODACTERIUM PHOSPHOREUM		54-89								AREA6
BETA CHAIN	VIBRIO FISCHERI		16-83								AREA7
BETA CHAIN	XENORHADDUS LUMINESCENS		39-69								AREA8
BETA CHAIN	PHOTODACTERIUM LEIOGNATHI		49-119	318-345							AREA9
BETA CHAIN	VIBRIO HAARVEI		10-37								AREA10
BETA CHAIN	PHOTODACTERIUM LEIOGNATHI		143-172								AREA11
BETA CHAIN	PHOTODACTERIUM PHOSPHOREUM		37-83	99-126							AREA12
BETA CHAIN	VIBRIO FISCHERI		137-148								AREA13
BETA CHAIN	VIBRIO HAARVEI		98-121								AREA14
BETA CHAIN	VIBRIO FISCHERI		10-38								AREA15
BETA CHAIN	PHOTODACTERIUM PHOSPHOREUM		10-37	162-189							AREA16
BETA CHAIN	VIBRIO HAARVEI		61-88								AREA17
BETA CHAIN	PHOTODACTERIUM LEIOGNATHI		288-295								AREA18
BETA CHAIN	PHOTODACTERIUM LEIOGNATHI		218-235								AREA19
BETA CHAIN	BACILLUS SUBTILIS		91-116								AREA20
BETA CHAIN	CLOSTRIDIUM ACETOBUTYLICUM		91-118								AREA21
BETA CHAIN	ESCHERICHIA COLI		142-176								AREA22
BETA CHAIN	BACILLUS SUBTILIS		55-82	150-177	467-513	535-581					AREA23
BETA CHAIN	ESCHERICHIA COLI		210-237								AREA24
BETA CHAIN	BACILLUS SUBTILIS		179-213	223-232							AREA25
BETA CHAIN	BACILLUS SUBTILIS		13-64	239-303							AREA26
BETA CHAIN	STREPTOCOCCUS PYOGENES		46-92	114-136	191-200	301-342	383-417	416-494			AREA27
BETA CHAIN	STREPTOCOCCUS PYOGENES		12-46	89-128	171-202	245-272	300-313	399-437			AREA28
BETA CHAIN	STREPTOCOCCUS PYOGENES		12-174	289-327							AREA29
BETA CHAIN	STREPTOCOCCUS PYOGENES		5-39	54-163	206-233	312-410					AREA30
BETA CHAIN	STREPTOCOCCUS PYOGENES		12-39	70-222	290-324	343-401					AREA31
BETA CHAIN	ESCHERICHIA COLI		70-47								AREA32
BETA CHAIN	ENTERODACTER AEROGENES		3-30								AREA33
BETA CHAIN	ENTERODACTER AEROGENES		932-979								AREA34
BETA CHAIN	ESCHERICHIA COLI		40-47	180-207							AREA35
BETA CHAIN	STREPTOCOCCUS PNEUMONIAE		410-441								AREA36
BETA CHAIN	CALDOCCELLUM SACCCHAROLYTICUM		389-427	592-636	1272-1276	1796-1722					AREA37
BETA CHAIN	BACILLUS STIGMATHII		246-273								AREA38
BETA CHAIN	ESCHERICHIA COLI		93-122								AREA39
BETA CHAIN	ESCHERICHIA COLI		38-43	100-114							AREA40
BETA CHAIN	WOLINELLA SUCCINQUEMENS		460-571								AREA41
BETA CHAIN	ESCHERICHIA COLI		47-78	122-163							AREA42
BETA CHAIN	ESCHERICHIA COLI		172-206	278-253	306-345						AREA43
BETA CHAIN	ESCHERICHIA COLI		372-399								AREA44
BETA CHAIN	ESCHERICHIA COLI		239-308								AREA45
BETA CHAIN	SALMONELLA TYPHIMURUM		219-306								AREA46
BETA CHAIN	ESCHERICHIA COLI		288-315								AREA47
BETA CHAIN	ESCHERICHIA COLI		111-149	164-191	277-304						AREA48
BETA CHAIN	ESCHERICHIA COLI		260-287	369-403	316-343						AREA49
BETA CHAIN	SALMONELLA TYPHIMURUM		314-348								AREA50
BETA CHAIN	ENTERODACTER AEROGENES		375-393								AREA51
BETA CHAIN	ENTERODACTER AEROGENES		41-48	158-208	317-351	488-523					AREA52
BETA CHAIN	ESCHERICHIA COLI		37-71								AREA53
BETA CHAIN	METHANOSARCINA BARKER		335-405								AREA54
BETA CHAIN	METHANOCOCCUS VOLTAELI		346-363								AREA55
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA56
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA57
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA58
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA59
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA60
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA61
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA62
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA63
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA64
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA65
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA66
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA67
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA68
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA69
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA70
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA71
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA72
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA73
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA74
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA75
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA76
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA77
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA78
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA79
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA80
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA81
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA82
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA83
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA84
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA85
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA86
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA87
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA88
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA89
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA90
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA91
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA92
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA93
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA94
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA95
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA96
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA97
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA98
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA99
BETA CHAIN	METHANOCOCCUS VOLTAELI		315-343								AREA100



PC GENE	1071-1114	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
PROTEIN	METHYL-COENZYME M REDUCTASE	METHANOTHERMABUS FERVIDUS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								



185



PCGENE	10/11/1984	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PCGENE	10/11/1984	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA3																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																



ECCLP	101176.4	Protein	Organism	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELLCLADIE	PROTEIN	ELLCLADIE	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PHIM BRAJA	BIOSYNTHESIS PROTEIN NIFN	BIOSYNTHESIS PROTEIN NIFN	BRADYRHIZOBIUM JAPONICUM	116-366								
PHIS ANASP	NIF S PROTEIN	NIF S PROTEIN	ANABAENA SP	112-139								
PHIS LACDE	NIF S PROTEIN HOMOLOG	NIF S PROTEIN HOMOLOG	LACTOBACILLUS DELBRUECKII	59-86								
PHIT AZOVI	NIF T PROTEIN	NIF T PROTEIN	AZOTOBACTER VINELANDII	6-33								
PHIU ANASL	NIF U PROTEIN	NIF U PROTEIN	ANABAENA SP	7-69								
PHIU ANASP	NIF U PROTEIN	NIF U PROTEIN	ANABAENA SP	148-178								
PHIU KLEPH	NIF U PROTEIN	NIF U PROTEIN	KLERSIELLA PNEUMONIAE	66-93								
PHIK ECOLI	NICKEL TRANSPORT PROTEIN NIK A PRECURSOR	NICKEL TRANSPORT PROTEIN NIK A PRECURSOR	ESCHERICHIA COLI	122-149	436-413							
PHIK ECOLI	NICKEL TRANSPORT PROTEIN NIK E	NICKEL TRANSPORT PROTEIN NIK E	ESCHERICHIA COLI	137-204								
PHILB ECOLI	NITRITE REDUCTASE	NITRITE REDUCTASE	ESCHERICHIA COLI	145-172								
PHIC ECOLI	NITR C PROTEIN	NITR C PROTEIN	ESCHERICHIA COLI	212-239								
PHIS PSEST	PSEUDOMONAS CYTOCHROME OXIDASE PRECURSOR	PSEUDOMONAS CYTOCHROME OXIDASE PRECURSOR	PSEUDOMONAS STUTZERI	303-333								
PHIB LACLA	117 KD MEMBRANE ASSOCIATED PROTEIN	117 KD MEMBRANE ASSOCIATED PROTEIN	LACTOCOCCUS LACTIS	302-239	663-697	886-970						
PHIS LACLA	NISIN BIOSYNTHESIS PROTEIN NISC	NISIN BIOSYNTHESIS PROTEIN NISC	LACTOCOCCUS LACTIS	32-92	140-188							
PHIS LACLA	NISIN TRANSPORT PROTEIN NIST	NISIN TRANSPORT PROTEIN NIST	LACTOCOCCUS LACTIS	223-233	278-305	476-470						
PHIV CLOPA	HOMOCITRATE SYNTHASE, ALPHA SUBUNIT	HOMOCITRATE SYNTHASE, ALPHA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	100-127	234-268							
PHIV CLOPA	HOMOCITRATE SYNTHASE, OMEGA SUBUNIT	HOMOCITRATE SYNTHASE, OMEGA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	63-94	103-132	213-240	283-310					
PHIV ECOLI	FOUR PROTEIN NADPC PRECURSOR	FOUR PROTEIN NADPC PRECURSOR	ESCHERICHIA COLI	32-49	69-96	235-262						
PHODC BRASP	MODULATION PROTEIN C	MODULATION PROTEIN C	BRADYRHIZOBIUM SP	3-30								
PHODC RHELO	MODULATION PROTEIN C	MODULATION PROTEIN C	RHIZOBIUM LOTI	286-313								
PHODC RHILV	MODULATION PROTEIN C	MODULATION PROTEIN C	RHIZOBIUM LEGUMINOSARUM	14-48								
PHODC RHILV	MODULATION PROTEIN F	MODULATION PROTEIN F	RHIZOBIUM LEGUMINOSARUM	31-58								
PHODC RHILV	MODULATION PROTEIN F	MODULATION PROTEIN F	RHIZOBIUM MELLEOTI	39-66								
PHODG RHIME	MODULATION PROTEIN G	MODULATION PROTEIN G	RHIZOBIUM MELLEOTI	8-33								
PHODG RHILV	MODULATION PROTEIN G	MODULATION PROTEIN G	RHIZOBIUM MELLEOTI	8-33								
PHODG RHILV	MODULATION PROTEIN L	MODULATION PROTEIN L	RHIZOBIUM LEGUMINOSARUM	26-33								
PHODG AZORA	MODULATION PROTEIN D	MODULATION PROTEIN D	AZOSPILLULUM BRAZILENSE	60-87								
PHODT RHILY	MODULATION PROTEIN Y	MODULATION PROTEIN Y	RHIZOBIUM LEGUMINOSARUM	104-134	355-382	470-494						
PHODT RHILV	MODULATION PROTEIN Y	MODULATION PROTEIN Y	RHIZOBIUM LEGUMINOSARUM	364-391	418-443							
PHODU RHIF	MODULATION PROTEIN U	MODULATION PROTEIN U	RHIZOBIUM FREDDI	506-536								
PHODV BRACA	MODULATION PROTEIN V	MODULATION PROTEIN V	BRADYRHIZOBIUM JAPONICUM	378-419	739-766							
PHODX RHILV	MODULATION PROTEIN X	MODULATION PROTEIN X	RHIZOBIUM LEGUMINOSARUM	232-239								
PHOLB RHIFR	MODULATION PROTEIN NOLB	MODULATION PROTEIN NOLB	RHIZOBIUM FREDDI	133-160								
PHOLB RHIFR	MODULATION PROTEIN NOLB	MODULATION PROTEIN NOLB	RHIZOBIUM MELLEOTI	88-113								
PHODS PSEST	MOD PROTEIN PRECURSOR	MOD PROTEIN PRECURSOR	PSEUDOMONAS STUTZERI	319-346								
PHODS PSEST	REGULATORY PROTEIN NOSR	REGULATORY PROTEIN NOSR	PSEUDOMONAS STUTZERI	137-154								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS AERUGINOSA	267-294								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS STUTZERI	553-591								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	BACILLUS AMYLOLQUEFACIENS	112-147	312-344							
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	BACILLUS POLYMYXA	37-91	107-228							
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	BACILLUS SUBTILIS	116-148	107-228							
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	PARACOCUS DENTRIFICANS	4-45								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	PARACOCUS DENTRIFICANS	125-133								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	ESCHERICHIA COLI	91-123								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	ESCHERICHIA COLI	319-346								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	ESCHERICHIA COLI	72-111								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	RHODOCOCCUS RHODOCITRUS	109-136	115-162							
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	LACTOCOCCUS LACTIS	52-79								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	ANABAENA SP	65-92								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	SYNECHOCOCCUS SP	44-91								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	SYNECHOCOCCUS SP	67-94								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	VIBRIO ALGINOLYTICUS	194-223								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	PROTEUS VULGARIS	35-412								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	RHIZOBIUM MELLEOTI	431-478								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	SYNECHOCOCCUS SP	80-107								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	SYNECHOCOCCUS SP	37-34								
PHODS PSEST	NITRITIC OXIDE REDUCTASE PRECURSOR	NITRITIC OXIDE REDUCTASE PRECURSOR	SYNECHOCOCCUS SP	616-641								



188



189



190



PCPGAME	10/11/1784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															



ECGENE	10111014	Proteolytic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
CLLNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PPDA CLOPE	PROTEIN A PRECURSOR	CLOSTRIDIUM PERFRINGENS	31-103						
PPSA ECOLI	PHOSPHOENOLPYRUVATE SYNTHASE	ESCHERICHIA COLI	49-76						
PPQ2 ACICA	COENZYME P40 SYNTHESIS PROTEIN II	ACINETOBACTER CALCOACETICUS	40-74						
PPCA ANAVA	CALCIUM DEPENDENT PROTEASE PRECURSOR	ANABASNA VARIABILIS	371-398						
PPCA THEAC	PROTEASOME ALPHA SUBUNIT	THECAPOPLASMA ACIDOPHILUM	88-115						
PPC ECOLI	TAIL-SPECIFIC PROTEASE PRECURSOR	ESCHERICHIA COLI	346-393						
PPET STAAU	PLASMIID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	118-192	364-367					
PPET STAAU	PLASMIID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	27-78	152-159					
PPAE LACPL	PLASMIID RECOMBINATION ENZYME	LACTOBACILLUS PLANTARUM	48-75	181-208	366-393				
PPAE LACPL	PLASMIID RECOMBINATION ENZYME	LACTOBACILLUS PLANTARUM	37-71	191-218					
PPAE BACLI	REGULATORY PROTEIN	BACILLUS LICTENIFORMIS	2-40						
PPAE BACSP	PLASMIID RECOMBINATION ENZYME	BACILLUS SP	181-214	288-245					
PPAE STRAG	PLASMIID RECOMBINATION ENZYME	STREPTOCOCCUS AGALACTIAE	283-219	323-239	420-454				
PPFA LISMO	LISTERIOLYSIN REGULATORY PROTEIN	LISTERIA MONOCYTOGENES	76-110	173-204					
PPFA ECOLI	PRIMOSOMAL PROTEIN N	ESCHERICHIA COLI	218-245						
PPRM BACSU	DNA PRIMASE	BACILLUS SUBTILIS	181-413						
PPRM BUCAP	DNA PRIMASE	BUCKNERIA APHIDICOLA	13-43	282-219					
PPRM CLOAB	DNA PRIMASE	CLOSTRIDIUM ACETOBUTYLICUM	87-114						
PPRM LACLA	DNA PRIMASE	LACTOCOCCUS LACTIS	269-296						
PPRM RICPR	DNA PRIMASE	BUCKNERIA PROWAZEKII	10-37	245-286	473-504	526-593			
PPRL DESDE	PRISMANE PROTEIN	DESULFOVIBRIO DESULFURICANS	30-37						
PPRL ACHLY	BETA-LYTIC METALLOENDOPEPTIDASE	ACHROMOBACTER LYTTICUS	117-244						
PPRL LYSYN	BETA-LYTIC METALLOENDOPEPTIDASE	LYSOBACTER ENZYMOGENES	121-148						
PPROT LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145	275-316					
PPROT LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145						
PPROA SERMA	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE	SERRATIA MARCESCENS	306-336						
PPROA STAAU	PROTEIN A PRECURSOR	STAPHYLOCOCCUS AUREUS	2-29						
PPROB SERMA	GLUTAMATE KINASE	SERRATIA MARCESCENS	7-34						
PPROB STRAG	PROTEIN B	STREPTOCOCCUS AGALACTIAE	38-45						
PPROC PSEAE	PYRROLINE-5-CARBOXYLATE REDUCTASE	PSEUDOMONAS AERUGINOSA	148-175						
PPROH BACSU	PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOL	BACILLUS SUBTILIS	300-337						
PPROP ECOLI	PROLINE/NETRAINE TRANSPORTER	ESCHERICHIA COLI	460-487						
PPROV ECOLI	PERIPHERAL MEMBRANE PROTEIN PROV	ESCHERICHIA COLI	24-34						
PPROV SALTU	PERIPHERAL MEMBRANE PROTEIN PROV	SALMONELLA TYPHIMURUM	170-197						
PPRBD ECOLI	PIRB PROTEIN	ESCHERICHIA COLI	282-309						
PPRBD ECOLI	ANTICODON NUCLEASE	ESCHERICHIA COLI	278-303						
PPRAD ECOLI	PIRD PROTEIN	BACILLUS SUBTILIS	32-87	95-137					
PPRA BACSU	PROTEIN EXPORT PROTEIN PRSA PRECURSOR	STREPTOMYCES GRISEUS	36-110						
PPRA STRGR	PROTEIN A PRECURSOR	ERWINIA CHRYSANTHEMI	107-120						
PPRIC ERWCH	SECRETED PROTEASE C PRECURSOR	PORPHYROMONAS GINGIVALIS	283-312						
PPRIC PORGI	COLLAGENASE PRECURSOR	ERWINIA CHRYSANTHEMI	128-155						
PPRID ERWCH	PROTEASES SECRETION PROTEIN PRID	ERWINIA CHRYSANTHEMI	106-133	219-265	346-344				
PPRIE DACNO	EXTRACELLULAR SERINE PROTEASE PRECURSOR	HAETEROPHYS NITROSUS	106-133	158-192	231-290				
PPRIE UNWCH	PROTEASES SECRETION PROTEIN PRTE	ERWINIA CHRYSANTHEMI	280-310						
PPRIF ERWCH	PROTEASES SECRETION PROTEIN PRIF	ERWINIA CHRYSANTHEMI	76-103	113-139					
PPRIM LACLA	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	26-33	36-103	112-139				
PPRIM LACLC	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	76-103	112-139					
PPRIM LACLA	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOBACILLUS PASTORIS	104-111	378-407	1007-1041				
PPRIM LACLA	PROTEASE MATURATION PROTEIN PRECURSOR	SERRATIA MARCESCENS	304-331	464-491	1007-1041				
PPRIS SERMA	EXTRACELLULAR SERINE PROTEASE PRECURSOR	ERWINIA CHRYSANTHEMI	314-341						
PPRIT SERMA	SECRETED PROTEASE C PRECURSOR	SYNCHOCOCUS ELONGATUS NAEGEL	170-187						
PPRIT ERWCH	CHLOROPHYLL A ANOPROTEIN A1	SYNCHOCOCUS SP	109-126	326-356					
PPSAA STRGR	CHLOROPHYLL A ANOPROTEIN A1	SYNCHOCOCUS SP	170-187						
PPSAA STRAU	CHLOROPHYLL A ANOPROTEIN A1	SYNCHOCOCUS SP	44-71	170-187	338-368				
PPSAI STRYJ	CHLOROPHYLL A ANOPROTEIN A1	YERSINIA PESTIS	244-271						
PPSAI YERPE	CHAPERONE PROTEIN PSAT PRECURSOR	SYNCHOCOCUS SP	11-38						
PPSAD SYMPE	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II	YERSINIA PESTIS	66-118						
PPSAE YERPE	PSAE PROTEIN PRECURSOR	YERSINIA PESTIS							



GENE	FUNCTION	Protein Sequence	ARAL	ARAL	ARAL	ARAL	ARAL	ARAL
ELRPAK1	PROTEIN	ORGANISM	ARAL	ARAL	ARAL	ARAL	ARAL	ARAL
PSBO ANAH	STABILIZING POLYPEPTIDE PRECURSOR	ANABACUS NIDULANS	55-81					
PSBA ECOL	PHAGE SHOCK PROTEIN A	ESCHERICHIA COLI	110-141					
PSKA WOLSU	POLYSULFIDE REDUCTASE CHAIN A PRECURSOR	WOLINELLA SUCCINIFERENS	40-74					
PSLS ECOL	PHOSPHATE BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	26-60					
PT11 BACSU	PHOSPHOTRANSFERASE	BACILLUS SUBTILIS	113-163	399-426				
PT11 ECOL	PHOSPHOTRANSFERASE	ESCHERICHIA COLI	212-319	399-426				
PT11 SALTU	PHOSPHOTRANSFERASE	SALMONELLA TYPHIMURUM	34-61					
PT11 STACA	PHOSPHOTRANSFERASE	STAPHYLOCOCCUS CARNOBACTRIUS	198-232					
PT11 STSRL	PHOSPHOTRANSFERASE	STREPTOCOCCUS SALIVARIUS	127-154					
PT11 TRACH	PHOSPHOTRANSFERASE ENZYME II	ERWINIA CHRYSANTHEMI	670-697					
PT11 BACSU	PHOSPHOTRANSFERASE ENZYME II	BACILLUS SUBTILIS	517-544					
PT11 LACCA	PHOSPHOTRANSFERASE ENZYME II	LACTOBACILLUS CASEI	181-214	409-416				
PT11 LACCA	PHOSPHOTRANSFERASE ENZYME II	LACTOCOCCUS LACTIS	421-448	530-537				
PT11 STAAU	PHOSPHOTRANSFERASE ENZYME II	STAPHYLOCOCCUS ALBUS	443-489					
PT11 ECOL	PHOSPHOTRANSFERASE ENZYME II	ESCHERICHIA COLI	388-415					
PT11 STACA	PHOSPHOTRANSFERASE ENZYME II	STAPHYLOCOCCUS CARNOBACTRIUS	170-200					
PT11 ECOL	N-ACETYLGLUCOSAMINE PHOSPHATASE	ESCHERICHIA COLI	609-637					
PT11 STRAU	PHOSPHOTRANSFERASE ENZYME II	STREPTOCOCCUS RUTANS	107-134					
PT11 SALTU	PHOSPHOTRANSFERASE FOR PROTEIN	SALMONELLA TYPHIMURUM	40-47					
PT11 LACCA	PHOSPHOTRANSFERASE FACTOR III	LACTOBACILLUS CASEI	11-65					
PT11 ECOL	PHOSPHOCARRIER PROTEIN HPA	ESCHERICHIA COLI	31-45					
PT11 ECOL	PHOSPHOCARRIER PROTEIN HPA	SALMONELLA TYPHIMURUM	94-121	213-231				
PT11 ECOL	PROTEASE II	ESCHERICHIA COLI	94-121	213-231				
PT11 ECOL	PULLULANASE	ESCHERICHIA COLI	994-928					
PT11 ECOL	PULLULANASE	KLBSIELLA AEROGES	194-218					
PT11 ECOL	LEADER PEPTIDASE	KLBSIELLA PNEUMONIAE	178-203					
PT11 ECOL	PULS PRECURSOR	KLBSIELLA PNEUMONIAE	10-97					
PT11 ECOL	UPTAKE PROTEIN PRECURSOR	PSEUDOMONAS PUTIDA	113-163	210-237	370-463			
PT11 BACSU	AMIDOPHOSPHORIBOSYL TRANSFERASE	BACILLUS SUBTILIS	394-421					
PT11 BACSU	PHOSPHORIBOSYLAMINE GLYCINE LIGASE	BACILLUS SUBTILIS	149-176					
PT11 BACSU	FORMYLTRANSFERASE	BACILLUS SUBTILIS	217-244					
PT11 ECOL	FORMYLTRANSFERASE	ESCHERICHIA COLI	18-43					
PT11 BACSU	SYNTHASE I	BACILLUS SUBTILIS	133-194					
PT11 BACSU	CYCLO-LIGASE	BACILLUS SUBTILIS	111-138					
PT11 ECOL	AIR CARBOXYLASE	ESCHERICHIA COLI	141					
PT11 BACSU	SACCHAR SYNTHETASE	BACILLUS SUBTILIS	226-233					
PT11 ECOL	ADENYLOSUCINATE LYASE	BACILLUS SUBTILIS	194-231	231-272				
PT11 ECOL	ADENYLOSUCINATE LYASE	BACILLUS SUBTILIS	18-53	245-272				
PT11 BACSU	ACAR TRANSFORMYLASE	ESCHERICHIA COLI	219-268					
PT11 ECOL	ACAR TRANSFORMYLASE	ESCHERICHIA COLI	218-267					
PT11 SALTU	ACAR TRANSFORMYLASE	SALMONELLA TYPHIMURUM	609-636					
PT11 BACSU	SYNTHASE II	BACILLUS SUBTILIS	18-115					
PT11 ANASP	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 MASLA	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 ANASP	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 MASLA	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 MASLA	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 ANASP	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 ANASP	LINKER POLYPEPTIDE CPGI	ANABACUS SP	18-115					
PT11 FREDI	31.6 KD LINKER POLYPEPTIDE	FRONTYELLA DIPLOSIPHON	105-132					
PT11 FREDI	31.6 KD LINKER POLYPEPTIDE	FRONTYELLA DIPLOSIPHON	22-46					
PT11 FREDI	31.6 KD LINKER POLYPEPTIDE	FRONTYELLA DIPLOSIPHON	106-143					
PT11 FREDI	31.6 KD LINKER POLYPEPTIDE	FRONTYELLA DIPLOSIPHON	41-70	113-140				
PT11 FREDI	31.6 KD LINKER POLYPEPTIDE	FRONTYELLA DIPLOSIPHON	9-36					
PT11 BACSU	ASPARTATE CARBAHOXYLTRANSFERASE	BACILLUS SUBTILIS	70-97					
PT11 SERMA	ASPARTATE CARBAHOXYLTRANSFERASE	SERRATIA MARCESCENS	113-142					
PT11 ECOL	DIBIOTRIBIOTINATE DEHYDROGENASE	ESCHERICHIA COLI	113-142					



194



PCCLONE	1974174.4	Protein Name	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PRMA STAP	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	336	81-108								
PRP1 ECOLI	REPLICATION PROTEIN REPA	ESCHERICHIA COLI	30-31	90-117								
PRPA BACSU	REPA PROTEIN	BACILLUS SUBTILIS	142-173	128-155								
PRPA ECOLI	REPA PROTEIN	ESCHERICHIA COLI	91-118	138-172								
PRPA PERGO	REPLICATION PROTEIN	NEISSERIA GONORRHOEAE	37-64									
PRPB LACPL	REPLICATION INITIATION PROTEIN	LACTOBACILLUS PLANTARUM	184-211									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	354-384									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	358-385									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	398-407									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	423-467									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	111-130	172-210								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	388-395									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	168-195	197-224	143-173							
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	119-148	205-243								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	119-199	260-287								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	68-102	151-185								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	34-48									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	84-113	183-204								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	84-113	183-204								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	180-210	443-473								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	199-228									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	185-212									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	37-66	237-268								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	84-95	145-172	210-261							
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	335-369									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	366-393									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	326-360									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	6-31									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	61-89	184-200								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	18-45									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	3-20	85-111								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	220-259									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	212-261									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	22-54	205-232								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	140-216									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	91-110									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	15-68	190-262	210-261							
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	175-202									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	175-202									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	10-41									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	152-179									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	206-233									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	118-163									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	215-242	327-369								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	82-109									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	667-694									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	380-414	667-694	1016-1081							
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	345-372	1071-1098								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	93-127									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	167-194									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	2-47	131-158								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	8-33									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	14-41									
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	14-72	106-133								
PRPB STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	2-34									



196



[illegible]



PLCLINE	10111744	Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
EULEMARI	PROLIN		4-31						
PR5B ANASP	RNA POLYMERASE SIGMA-B FACTOR		5-33	109-196					
PR5B BACSU	RNA POLYMERASE SIGMA-B FACTOR		41-74						
PR5B NITAXU	RNA POLYMERASE SIGMA-B FACTOR		98-133						
PR5B ANASP	RNA POLYMERASE SIGMA-C FACTOR		58-83						
PR5B BACSU	RNA POLYMERASE SIGMA-C FACTOR		192-249						
PR5B ANASP	RNA POLYMERASE SIGMA-D FACTOR		61-90						
PR5B BACSU	RNA POLYMERASE SIGMA-E FACTOR		14-41	116-160					
PR5B BACSU	RNA POLYMERASE SIGMA-F FACTOR		191-223	191-248					
PR5B BACSU	RNA POLYMERASE SIGMA-F FACTOR		4-31	191-248					
PR5B BACSU	RNA POLYMERASE SIGMA-F FACTOR		191-218						
PR5B BACSU	RNA POLYMERASE SIGMA-H FACTOR		116-217						
PR5B BACSU	RNA POLYMERASE SIGMA-H FACTOR		71-109	189-216					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		19-46						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		232-273						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		31-60						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		8-42						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		44-83						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		14-73	144-171					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		98-126	387-392	149-176				
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		91-125	172-217					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		1-28						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		91-125						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		81-110						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		77-108	136-163					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		50-77						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		166-187						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		31-62	187-216					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		16-43						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		69-94						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		32-49						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		101-110						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		41-78						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		80-107						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		235-268						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		175-202	314-381					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		175-202	314-381					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		31-45	153-189	314-369				
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		101-139	188-216					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		394-231	343-310					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		150-177						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		17-47						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		31-58						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		37-44						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		216-266	317-364	315-353	627-636	178-812	821-865	913-942
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		177-164	314-397					
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		3-32	416-470	531-580				
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		38-55						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		126-160	784-811	831-810				
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		174-201						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		182-217	314-383	391-422				
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		315-342						
PR5B BACSU	RNA POLYMERASE SIGMA-K FACTOR		93-124						



199



200



[illegible]



202



GENE	1071714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
FILENAME	PROTIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PTHER BACTH	THERMOLYSIN	BACILLUS THERMOPROTEOLYTICUS	86-113											
PTHER THEVU	THERMOLYSIN	THERMOACTINOMYCES VULGARIS	131-161											
PTHER ECOLI	THERMOLYSIN	ESCHERICHIA COLI	312-263	301-318										
PTHER ECOLI	THIIC PROTEIN	ESCHERICHIA COLI	138-163											
PTHER ECOLI	THIIC PROTEIN	ESCHERICHIA COLI	131-172	199-213										
PTHER SULAC	THIOPHOSIN PRECURSOR	SULFOLOBUS ACIDOCALDARIUS	288-315											
PTHER BIELA	THIOPHOSIN PRECURSOR	BREVIBACTERIUM LACTOFLAVENTUM	69-96											
PTHER SACER	PUTATIVE THIOLACTATE SULFURTRANSFERASE	SACCHAROPOLYSPORA ERYTHRAEA	144-171											
PTHER ECOLI	TRIGGER FACTOR	ESCHERICHIA COLI	216-266											
PTHER TREPA	TREPONEMAL MEMBRANE PROTEIN A PRECURSOR	TREPONEMA PALLIDUM	44-71											
PTHER TREPA	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PALLIDUM	41-68											
PTHER TREPH	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PHAGEDENIS	74-108											
PTHER ECOLI	LOW AFFINITY TRYPTOPHAN PEPTIDASE	ESCHERICHIA COLI	51-79	312-349										
PTHER STAAL	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	59-97	111-138										
PTHER ENTRA	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	131-178											
PTHER STAAL	TRANSPOSASE A	STAPHYLOCOCCUS AUREUS	589-615											
PTHER STAAL	TRANSPOSASE B	STAPHYLOCOCCUS AUREUS	7-43	174-201										
PTHER BACTU	THP TRANSOLVASE	BACILLUS THURINGIENSIS	99-126	316-337										
PTHER ECOLI	TRANSPOSON TNY7 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	312-39	316-341										
PTHER ECOLI	TRANSPOSON TNY7 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	316-366											
PTHER ECOLI	TRANSPOSON TNY7 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	463-490											
PTHER ECOLI	TRANSPOSON TNY7 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	36-63											
PTHER PSEPU	TOLUENE 1,2-DIOXYGENASE ALPHA SUBUNIT	PSEUDOMONAS PUTIDA	119-153											
PTHER PSEPU	TOLUENE 1,2-DIOXYGENASE BETA SUBUNIT	PSEUDOMONAS PUTIDA	179-213											
PTHER PSEPU	TOLUENE 1,2-DIOXYGENASE SYSTEM	PSEUDOMONAS PUTIDA	141-170											
PTHER PSEPU	TODX PRODUCT HYDROLASE	PSEUDOMONAS PUTIDA	101-138											
PTHER ECOLI	TOLA PROTEIN	ESCHERICHIA COLI	144-178	316-337										
PTHER ECOLI	OUTER MEMBRANE PROTEIN TOLC PRECURSOR	ESCHERICHIA COLI	201-230											
PTHER ECOLI	DNA TOPOISOMERASE I	SYNCHOCOCUS SP	397-424											
PTHER ECOLI	TRIMETHYLAMINE-N-OXIDE REDUCTASE	ESCHERICHIA COLI	179-208											
PTHER BORPE	PENTUSSIS TOXIN SUBUNIT I (S1) PRECURSOR	BORDETELLA PERTUSSIS	58-85											
PTHER CLOOT	PENTUSSIS TOXIN SUBUNIT 2 (S2) PRECURSOR	BORDETELLA PERTUSSIS	20-48											
PTHER PREAE	EXOTOXIN A PRECURSOR	CLOSTRIDIUM DIFFICILE	470-497											
PTHER CLODI	EXOTOXIN B	CLOSTRIDIUM DIFFICILE	18-72	133-163										
PTHER VIBCH	TRANSMEMBRANE REGULATORY PROTEIN TOX5	VIBRIO CHOLERAE	13-40											
PTHER TREPA	ANTIGEN TPFI	TREPONEMA PALLIDUM	106-141											
PTHER ECOLI	TRIOSEPHOSPHATE ISOMERASE	ESCHERICHIA COLI	81-110											
PTHER MORSP	TRIOSEPHOSPHATE ISOMERASE	MORAXELLA SP	136-164											
PTHER PORGI	THIOL PROTEINASE PRECURSOR	PORPHYROMONAS GINGIVALIS	117-144											
PTHER AGRT4	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	319-344	501-519										
PTHER PSESS	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	319-366	501-519										
PTHER STAAL	TRANSPOSASE	PSEUDOMONAS SYRINGAE	41-48											
PTHER STAAL	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	58-113											
PTHER STAAL	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	11-38	58-113										
PTHER STAAL	TRANSPOSASE	ESCHERICHIA COLI	321-355											
PTHER ECOLI	TRANSPOSASE	MUTAZOBACTERIUM MELLITUM	179-208											
PTHER ECOLI	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	31-40	64-93										
PTHER ECOLI	TRANSPOSASE	ESCHERICHIA COLI	181-208	108-140										
PTHER ECOLI	TRANSPOSASE	ESCHERICHIA COLI	31-78											
PTHER SHRO	TRANSPOSASE	BRIGELLA SONNEI	51-78	200-227										
PTHER ECOLI	TRANSPOSASE	ESCHERICHIA COLI	321-355											
PTHER MYCTU	PUTATIVE TRANSPOSASE	MYCOBACTERIUM TUBERCULOSIS	321-355											
PTHER BACTB	ISD1B PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	159-186											
PTHER BACTB	ISD1B PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	381-308	419-446										
PTHER STAAL	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	431	419-446										
PTHER BACTB	ISD1B PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446										
PTHER BACTB	TRANSPOSASE	BACILLUS THURINGIENSIS	91-127	509-539										



204



FCGENE	10/17/04	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
ORGANISM																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										



206



CCGEME	total184d	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000	AREA.1001	AREA.1002	AREA.1003	AREA.1004	AREA.1005	AREA.1006	AREA.1007	AREA.1008	AREA.1009	AREA.1010	AREA.1011	AREA.1012	AREA.1013	AREA.1014	AREA.1015	AREA.1016	AREA.1017	AREA.1018	AREA.1019	AREA.1020	AREA.1021	AREA.1022	AREA.1023	AREA.1024	AREA.1025	AREA.1026	AREA.1027	AREA.1028	AREA.1029	AREA.1030	AREA.1031	AREA.1032	AREA.1033	AREA.1034	AREA.1035	AREA.1036	AREA.1037	AREA.1038	AREA.1039	AREA.1040	AREA.1041	AREA.1042	AREA.1043	AREA.1044	AREA.1045	AREA.1046	AREA.1047	AREA.1048	AREA.1049	AREA.1050	AREA.1051	AREA.1052	AREA.1053	AREA.1054	AREA.1055	AREA.1056	AREA.1057	AREA.1058	AREA.1059	AREA.1060	AREA.1061	AREA.1062	AREA.1063	AREA.1064	AREA.1065	AREA.1066	AREA.1067	AREA.1068	AREA.1069	AREA.1070	AREA.1071	AREA.1072	AREA.1073	AREA.1074	AREA.1075	AREA.1076	AREA.1077	AREA.1078	AREA.1079	AREA.1080	AREA.1081	AREA.1082	AREA.1083	AREA.1084	AREA.1085	AREA.1086	AREA.1087	AREA.1088	AREA.1089	AREA.1090	AREA.1091	AREA.1092	AREA.1093	AREA.1094	AREA.1095	AREA.1096	AREA.1097	AREA.1098	AREA.1099	AREA.1100	AREA.1101	AREA.1102	AREA.1103	AREA.1104	AREA.1105	AREA.1106	AREA.1107	AREA.1108	AREA.1109	AREA.1110	AREA.1111	AREA.1112	AREA.1113	AREA.1114	AREA.1115	AREA.1116	AREA.1117	AREA.1118	AREA.1119	AREA.1120	AREA.1121	AREA.1122	AREA.1123	AREA.1124	AREA.1125	AREA.1126	AREA.1127	AREA.1128	AREA.1129	AREA.1130	AREA.1131	AREA.1132	AREA.1133	AREA.1134	AREA.1135	AREA.1136	AREA.1137	AREA.1138	AREA.1139	AREA.1140	AREA.1141	AREA.1142	AREA.1143	AREA.1144	AREA.1145	AREA.1146	AREA.1147	AREA.1148	AREA.1149	AREA.1150	AREA.1151	AREA.1152	AREA.1153	AREA.1154	AREA.1155	AREA.1156	AREA.1157	AREA.1158	AREA.1159	AREA.1160	AREA.1161	AREA.1162	AREA.1163	AREA.1164	AREA.1165	AREA.1166	AREA.1167	AREA.1168	AREA.1169	AREA.1170	AREA.1171	AREA.1172	AREA.1173	AREA.1174	AREA.1175	AREA.1176	AREA.1177	AREA.1178	AREA.1179	AREA.1180	AREA.1181	AREA.1182	AREA.1183	AREA.1184	AREA.1185	AREA.1186	AREA.1187	AREA.1188	AREA.1189	AREA.1190	AREA.1191	AREA.1192	AREA.1193	AREA.1194	AREA.1195	AREA.1196	AREA.1197	AREA.1198	AREA.1199	AREA.1200	AREA.1201	AREA.1202	AREA.1203	AREA.1204	AREA.1205	AREA.1206	AREA.1207	AREA.1208	AREA.1209	AREA.1210	AREA.1211	AREA.1212	AREA.1213	AREA.1214	AREA.1215	AREA.1216	AREA.1217	AREA.1218	AREA.1219	AREA.1220	AREA.1221	AREA.1222	AREA.1223	AREA.1
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208



209



GENE	10211814	Proteomic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	ORGANISM							
PYCE ECOLI	HYPOTHETICAL 603 KD PROTEIN	ESCHERICHIA COLI	434-411						
PYCO ECOLI	HYPOTHETICAL 593 KD PROTEIN	ESCHERICHIA COLI	394-471						
PYCO ECOLI	HYPOTHETICAL 331 KD PROTEIN	ESCHERICHIA COLI	91-118						
PYCP ECOLI	HYPOTHETICAL 514 KD PROTEIN	ESCHERICHIA COLI	343-369						
PYCS ECOLI	HYPOTHETICAL 717 KD PROTEIN	ESCHERICHIA COLI	366-396						
PYCW ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	50-84						
PYDA ECOLI	HYPOTHETICAL 843 KD PROTEIN	ESCHERICHIA COLI	3-29	551-485					
PYDB ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	103-134						
PYJA ECOLI	HYPOTHETICAL 173 KD PROTEIN PRECURSOR	ESCHERICHIA COLI	35-49	18-179					
PYKB BAG9	HYPOTHETICAL 488 KD PROTEIN	BACILLUS FINNIS	321-355						
PYLA1 LACAC	HYPOTHETICAL PROTEIN	LACTOBACILLUS ACIDOPHILUS	67-74						
PYLA3 LACAC	HYPOTHETICAL 143 KD PROTEIN	LACTOBACILLUS ACIDOPHILUS	13-43						
PYLA3 LACAC	HYPOTHETICAL 144 KD PROTEIN	LACTOBACILLUS ACIDOPHILUS	47-74						
PYLAC SULSO	HYPOTHETICAL 344 KD PROTEIN	SULFOLOBUS SOLFATARICUS	35-50						
PLY1 PSEU	HYPOTHETICAL 447 KD PROTEIN	PSEUDOMONAS PUTIDA	186-213	314-341					
PLYA YEREN	YLP4 LIPOPROTEIN PRECURSOR	YERSINIA ENTEROCOLITICA	184-221						
PLYD ANAYA	HYPOTHETICAL 316 KD PROTEIN	ANABAENA VARIABILIS	177-199						
PLYD LACLA	HYPOTHETICAL 297 KD PROTEIN	LACTOCOCCUS LACTIS	35-70						
PLYM3 BACSU	HYPOTHETICAL 313 KD PROTEIN	BACILLUS SUBTILIS	52-78						
PLYM3 MYCGE	HYPOTHETICAL 114 KD PROTEIN PRECURSOR	MYCOPLASMA GENITALIUM	36-83	159-193	420-445	581-1008			
PLYM3 CLOPE	HYPOTHETICAL PROTEIN	CLOSTRIDIUM PERFRINGENS	139-166						
PLYM3 CLOPE	HYPOTHETICAL 312 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	12-49	61-97	182-211				
PLYM1 METL	HYPOTHETICAL PROTEIN	METHANOCOCCUS THERMOLITHOTROPICUS	51-89						
PLYM1 FANDE	HYPOTHETICAL 93 KD PROTEIN	PARACOCOCUS DENITRIFICANS	52-84						
PLYM1 ANAS3	HYPOTHETICAL 211 KD PROTEIN	ANABAENA SP	171-198						
PLYM1 ANAS3	HYPOTHETICAL 211 KD PROTEIN	ANABAENA SP	37-165						
PLYM1 ANAS3	HYPOTHETICAL 314 KD PROTEIN	ESCHERICHIA COLI	5-32						
PLYM1 ECOLI	HYPOTHETICAL 413 KD PROTEIN	ESCHERICHIA COLI	104-171	289-316					
PLYM1 ECOLI	HYPOTHETICAL 139 KD PROTEIN	ESCHERICHIA COLI	12-44						
PLYM1 ECOLI	HYPOTHETICAL 913 KD PROTEIN	ESCHERICHIA COLI	371-248						
PLYM1 ECOLI	HYPOTHETICAL 913 KD PROTEIN	ESCHERICHIA COLI	41-42						
PLYM1 ECOLI	HYPOTHETICAL 913 KD PROTEIN	ESCHERICHIA COLI	143-193						
PLYM1 ECOLI	HYPOTHETICAL 543 KD PROTEIN	ESCHERICHIA COLI	94-121						
PLYM1 ECOLI	HYPOTHETICAL 181 KD PROTEIN	ESCHERICHIA COLI	31-39						
PLYM1 PHOS9	HYPOTHETICAL PROTEIN IN OMPH1 REGION	PHOTOBACTERIUM SP	61-103						
PLYM1 YEREN	PROTEIN-TYROSINE PHOSPHATASE YOPH	YERSINIA ENTEROCOLITICA	61-103						
PLYM1 YEREN	PROTEIN-TYROSINE PHOSPHATASE YOPH	YERSINIA PSEUDOTUBERCULOSIS	61-103						
PLYM1 YEREN	OUTER MEMBRANE PROTEIN YOPN	YERSINIA ENTEROCOLITICA	21-50	66-91	233-263				
PLYM1 YEREN	OUTER MEMBRANE PROTEIN YOPN	YERSINIA PSEUDOTUBERCULOSIS	21-50	66-91	233-263				
PLYM1 YEREN	OUTER MEMBRANE PROTEIN YOPN	YERSINIA ENTEROCOLITICA	61-88						
PLYM1 YEREN	YOPD PROTEIN PRECURSOR	HAEMOPHILUS INFLUENZAE	142-174						
PLYM1 YEREN	HYPOTHETICAL 311 KD PROTEIN	HAEMOPHILUS INFLUENZAE	12-27						
PLYM1 LISAO	HYPOTHETICAL 319 KD PROTEIN	LISTERIA MONOCYTOGENES	187-210						
PLYM1 PYRWO	HYPOTHETICAL 247 KD PROTEIN	PYROCOCCUS WOESSEI	39-66						
PLYM1 HAEN	HYPOTHETICAL 198 KD PROTEIN	HAEMOPHILUS INFLUENZAE	49-79						
PLYM1 HAEN	HYPOTHETICAL 199 KD PROTEIN	HAEMOPHILUS INFLUENZAE	47-74	82-109					
PLYM1 HAEN	1 KD PROTEIN	HAEMOPHILUS INFLUENZAE	199-229						
PLYM1 HAEN	24 KD PROTEIN	HAEMOPHILUS INFLUENZAE	7-14						
PLYM1 HAEN	HYPOTHETICAL 137 KD PROTEIN	HAEMOPHILUS INFLUENZAE	416-450	688-722					
PLYM1 HAEN	93 KD PROTEIN	BACILLUS SUBTILIS	148-175						
PLYM1 BACSU	HYPOTHETICAL 34 KD PROTEIN	PROCOCCUS WOESSEI	66-91						
PLYM1 PYRWO	HYPOTHETICAL PROTEIN	LISTERIA MONOCYTOGENES	37-54						
PLYM1 LISAO	HYPOTHETICAL 189 KD PROTEIN	STAPHYLOCOCCUS AUREUS	110-137						
PLYM1 STAAU	HYPOTHETICAL 153 KD PROTEIN	BACILLUS SUBTILIS	57-84						
PLYM1 BALSJ	HYPOTHETICAL 323 KD PROTEIN	STAPHYLOCOCCUS AUREUS	39-70						
PLYM1 STAAU	HYPOTHETICAL 323 KD PROTEIN	STAPHYLOCOCCUS AUREUS	34-104						
PLYM1 STAAU	HYPOTHETICAL 389 KD PROTEIN	STAPHYLOCOCCUS AUREUS	32-40	62-89	179-206				
PLYM1 STAAU	HYPOTHETICAL 370 KD PROTEIN	STAPHYLOCOCCUS AUREUS	13-43	179-176					



PGCENE	10/11/2014	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PROTEIN	PROTEIN	AGROBACTERIUM TUMEFACIENS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								



PCGENE	ID#	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN									
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	ORGANISMI	244-271	279-304						
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS								
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	LEPTOSPIRA BIFLEXA	94-117							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	LACTOCOCCUS LACTIS	76-112							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	37-64							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	SPHILOPLASMA CITRI	102-149							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	37-64	69-91						
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	142-169							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	17-31							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	163-207	202-249						
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	3-30	34-41	94-143					
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	36-83	85-112						
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	24-38							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	ANABENA SP	77-104							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN		6-19							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	CALDOCELLUM SACCHAROLYTICUM	41-84							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	CALDOCELLUM SACCHAROLYTICUM	41-84							
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	ESCHERICHIA COLI	41-78							



TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS



214



215



PROTEIN	1011111111 Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ADAM10	ADAM10 (MEMBRANE TYPE 1 METALLOPROTEIN)	145-172	417-451	814-861	1795-1823	3172-3213	3372-3609		
ADAM11	ADAM11 (MEMBRANE TYPE 1 METALLOPROTEIN)	48-81	207-274						
ADAM12	ADAM12 (MEMBRANE TYPE 1 METALLOPROTEIN)	4468-4475							
ADAM13	ADAM13 (MEMBRANE TYPE 1 METALLOPROTEIN)	323-331							
ADAM14	ADAM14 (MEMBRANE TYPE 1 METALLOPROTEIN)	69-103							
ADAM15	ADAM15 (MEMBRANE TYPE 1 METALLOPROTEIN)	323-350							
ADAM16	ADAM16 (MEMBRANE TYPE 1 METALLOPROTEIN)	313-343	303-332						
ADAM17	ADAM17 (MEMBRANE TYPE 1 METALLOPROTEIN)	398-333							
ADAM18	ADAM18 (MEMBRANE TYPE 1 METALLOPROTEIN)	7-34							
ADAM19	ADAM19 (MEMBRANE TYPE 1 METALLOPROTEIN)	7-34							
ADAM20	ADAM20 (MEMBRANE TYPE 1 METALLOPROTEIN)	311-338	347-374						
ADAM21	ADAM21 (MEMBRANE TYPE 1 METALLOPROTEIN)	163-190							
ADAM22	ADAM22 (MEMBRANE TYPE 1 METALLOPROTEIN)	163-190							
ADAM23	ADAM23 (MEMBRANE TYPE 1 METALLOPROTEIN)	203-230							
ADAM24	ADAM24 (MEMBRANE TYPE 1 METALLOPROTEIN)	155-183							
ADAM25	ADAM25 (MEMBRANE TYPE 1 METALLOPROTEIN)	30-61							
ADAM26	ADAM26 (MEMBRANE TYPE 1 METALLOPROTEIN)	14-68							
ADAM27	ADAM27 (MEMBRANE TYPE 1 METALLOPROTEIN)	351-394							
ADAM28	ADAM28 (MEMBRANE TYPE 1 METALLOPROTEIN)	178-183							
ADAM29	ADAM29 (MEMBRANE TYPE 1 METALLOPROTEIN)	114-141							
ADAM30	ADAM30 (MEMBRANE TYPE 1 METALLOPROTEIN)	292-319	343-372						
ADAM31	ADAM31 (MEMBRANE TYPE 1 METALLOPROTEIN)	1081-1111							
ADAM32	ADAM32 (MEMBRANE TYPE 1 METALLOPROTEIN)	113-143	531-563	609-636					
ADAM33	ADAM33 (MEMBRANE TYPE 1 METALLOPROTEIN)	106-140							
ADAM34	ADAM34 (MEMBRANE TYPE 1 METALLOPROTEIN)	126-143	310-337	373-407					
ADAM35	ADAM35 (MEMBRANE TYPE 1 METALLOPROTEIN)	178-205							
ADAM36	ADAM36 (MEMBRANE TYPE 1 METALLOPROTEIN)	31-43							
ADAM37	ADAM37 (MEMBRANE TYPE 1 METALLOPROTEIN)	784-833							
ADAM38	ADAM38 (MEMBRANE TYPE 1 METALLOPROTEIN)	246-280	504-531						
ADAM39	ADAM39 (MEMBRANE TYPE 1 METALLOPROTEIN)	314-350							
ADAM40	ADAM40 (MEMBRANE TYPE 1 METALLOPROTEIN)	203-229							
ADAM41	ADAM41 (MEMBRANE TYPE 1 METALLOPROTEIN)	274-301							
ADAM42	ADAM42 (MEMBRANE TYPE 1 METALLOPROTEIN)	192-219							
ADAM43	ADAM43 (MEMBRANE TYPE 1 METALLOPROTEIN)	284-311							
ADAM44	ADAM44 (MEMBRANE TYPE 1 METALLOPROTEIN)	168-193							
ADAM45	ADAM45 (MEMBRANE TYPE 1 METALLOPROTEIN)	10-37							
ADAM46	ADAM46 (MEMBRANE TYPE 1 METALLOPROTEIN)	128-162	333-385						
ADAM47	ADAM47 (MEMBRANE TYPE 1 METALLOPROTEIN)	76-57							
ADAM48	ADAM48 (MEMBRANE TYPE 1 METALLOPROTEIN)	330-363							
ADAM49	ADAM49 (MEMBRANE TYPE 1 METALLOPROTEIN)	911-948							
ADAM50	ADAM50 (MEMBRANE TYPE 1 METALLOPROTEIN)	126-150							
ADAM51	ADAM51 (MEMBRANE TYPE 1 METALLOPROTEIN)	141-168							
ADAM52	ADAM52 (MEMBRANE TYPE 1 METALLOPROTEIN)	27-54							
ADAM53	ADAM53 (MEMBRANE TYPE 1 METALLOPROTEIN)	723-750							
ADAM54	ADAM54 (MEMBRANE TYPE 1 METALLOPROTEIN)	318-363							
ADAM55	ADAM55 (MEMBRANE TYPE 1 METALLOPROTEIN)	94-122	331-340						
ADAM56	ADAM56 (MEMBRANE TYPE 1 METALLOPROTEIN)	384-411	380-407						
ADAM57	ADAM57 (MEMBRANE TYPE 1 METALLOPROTEIN)	2-39							
ADAM58	ADAM58 (MEMBRANE TYPE 1 METALLOPROTEIN)	140-167							
ADAM59	ADAM59 (MEMBRANE TYPE 1 METALLOPROTEIN)	297-324	467-494						
ADAM60	ADAM60 (MEMBRANE TYPE 1 METALLOPROTEIN)	561-588							
ADAM61	ADAM61 (MEMBRANE TYPE 1 METALLOPROTEIN)	502-529							
ADAM62	ADAM62 (MEMBRANE TYPE 1 METALLOPROTEIN)	874-901							
ADAM63	ADAM63 (MEMBRANE TYPE 1 METALLOPROTEIN)	13-40							
ADAM64	ADAM64 (MEMBRANE TYPE 1 METALLOPROTEIN)	111-138	163-197	321-355					



217



[illegible]



[illegible]



PGCONE	1071114c Moll Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
POLY2 HUMAN	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL (EC 2.3.1.1) (SERINE)	417-444						
POLY3 HUMAN	18 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN	598-633						
POLY4 HUMAN	GLYCINE RECEPTOR ALPHA-2 CHAIN PRECURSOR	162-169						
POLY5 HUMAN	GRAVIN (FRAGMENT)	9-43						
POLY6 HUMAN	GROWTH HORMONE-RELEASING HORMONE RECEPTOR PRECURSOR (GHRII RECEPT	118-155						
POLY7 HUMAN	GLUTATHIONE S-TRANSFERASE MA SUBUNIT 2 (EC 2.3.1.18) (GTH2) (CLASS-	64-91						
POLY8 HUMAN	GLUTATHIONE S-TRANSFERASE MA SUBUNIT 1 (EC 2.3.1.18) (GTH1) (CLASS-	1012-1047						
POLY9 HUMAN	GTPASE-ACTIVATING PROTEIN (GAP) (GAS P21) PROTEIN ACTIVATOR	414-501						
POLY10 HUMAN	GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN	274-301						
POLY11 HUMAN	GLUCOSE TRANSPORTER TYPE 1, BRAIN	272-299						
POLY12 HUMAN	GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE	290-317						
POLY13 HUMAN	HISTONE H1	44-89						
POLY14 HUMAN	HISTONE H1A (H1.1)	71-104						
POLY15 HUMAN	HISTONE H1B (H1.4)	70-101						
POLY16 HUMAN	HISTONE H1C (H1.3)	71-102						
POLY17 HUMAN	HISTONE H1D (H1.2)	70-101						
POLY18 HUMAN	HISTONE H1E	74-105						
POLY19 HUMAN	HISTONE H2B.1	20-47						
POLY20 HUMAN	HISTONE H2B.2	20-47						
POLY21 HUMAN	HISTONE H2B (H2B.1 A)	20-47						
POLY22 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ-B1) ALPHA CHAIN PRECURSOR	142-169						
POLY23 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ-B1) BETA CHAIN PRECURSOR	50-83						
POLY24 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ-B1) BETA CHAIN PRECURSOR	50-77						
POLY25 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ-B1) BETA CHAIN PRECURSOR	50-77						
POLY26 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ-B1) BETA CHAIN PRECURSOR	10-43						
POLY27 HUMAN	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HBGF-1) (ACIDIC FIBROBLAST	102-129						
POLY28 HUMAN	HBGF-1 PROTO-ONCOGENE PROTEIN PRECURSOR (HBGF-1)	61-91						
POLY29 HUMAN	FIBROBLAST GROWTH FACTOR 4 PRECURSOR (FGF-4) (HBGF-4) (HST-2)	41-75	150-186					
POLY30 HUMAN	P59 PROTEIN (RSP BINDING DOCKING PROTEIN) (RBP) (POSSIBLE PEPTIDYL-PROLYL	244-312						
POLY31 HUMAN	URICOPHYLLIN-III SYNTHASE (EC 4.1.1.15) (URICOPHYLLIN-III)	74-118						
POLY32 HUMAN	HEPARIN COW FACTOR II PRECURSOR (HC-II) (PROTEASE INHIBITOR LEUSEPIN 1)	169-196						
POLY33 HUMAN	SERINE PROTEASE NEPAIN (EC 3.4.21.1)	22-49						
POLY34 HUMAN	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.32) (N-ACETYL-	316-383						
POLY35 HUMAN	BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.32) (N-ACETYL-BETA-	318-413						
POLY36 HUMAN	HOMEOBOX PROTEIN MSX-1 (HOX-7)	178-212						
POLY37 HUMAN	HEPATOCYTE NUCLEAR FACTOR 1 (HNF-1) (LIVER SPECIFIC	2-39						
POLY38 HUMAN	HEPATOXYGENASE 1 (EC 1.14.99.3) (HO-1)	197-224						
POLY39 HUMAN	4-HYDROXYBENZOYLGLUTAMATE DIOXYGENASE (EC 1.11.1.27) (4HPPD)	308-333						
POLY40 HUMAN	ZINC FINGER PROTEIN HIX	521-548	914-974	1037-1066	2215-2286	2289-2316	2317-2344	2448-2475
POLY41 HUMAN	HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN	43-70						
POLY42 HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 90)	443-470	640-674					
POLY43 HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 90)	511-543						
POLY44 HUMAN	HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR	113-140	168-209					
POLY45 HUMAN	HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR	117-198						
POLY46 HUMAN	10 HEAVY CHAIN PRECURSOR V-J REGION (AHL-7)	63-108						
POLY47 HUMAN	10 HEAVY CHAIN V-III REGION (GAL)	47-74						
POLY48 HUMAN	HOMEOBOX PROTEIN HOX-11 (H11) (PROTO-ONCOGENE)	282-289						
POLY49 HUMAN	HOMEOBOX PROTEIN HOX-8 (H8) (H8C) (H8D) (H8E)	135-163						
POLY50 HUMAN	ISLET AMYLOID POLYPEPTIDE	51-80						
POLY51 HUMAN	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-3)	112-210						
POLY52 HUMAN	PLASMA PROTEINASE C1 INHIBITOR PRECURSOR (C1 INH)	311-378						
POLY53 HUMAN	INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR (ICAM-2)	37-84						
POLY54 HUMAN	INSULIN DEGRADING ENZYME (EC 3.4.99.4) (INSULINASE) (INSULIN	474-504	607-641					
POLY55 HUMAN	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A)	212-249						
POLY56 HUMAN	INTRINSIC FACTOR PRECURSOR (IF) (GASTRIC INTRINSIC FACTOR)	149-178	408-433					
POLY57 HUMAN	INTRIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID	308-349						
POLY58 HUMAN	INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMATOPOIETIN-1)	80-107	103-210					
POLY59 HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE 1 PRECURSOR (IL-1R1) (P80)	76-110	172-199					



221



GENE	10017162 Mail Search on All Human Protein Sequences	ARKA1	ARKA2	ARKA3	ARKA4	ARKA5	ARKA6	ARKA7	ARKA8	ARKA9	ARKA10	ARKA11	ARKA12	ARKA13	ARKA14	ARKA15	ARKA16	ARKA17	ARKA18	ARKA19	ARKA20	ARKA21	ARKA22	ARKA23	ARKA24	ARKA25	ARKA26	ARKA27	ARKA28	ARKA29	ARKA30	ARKA31	ARKA32	ARKA33	ARKA34	ARKA35	ARKA36	ARKA37	ARKA38	ARKA39	ARKA40	ARKA41	ARKA42	ARKA43	ARKA44	ARKA45	ARKA46	ARKA47	ARKA48	ARKA49	ARKA50	ARKA51	ARKA52	ARKA53	ARKA54	ARKA55	ARKA56	ARKA57	ARKA58	ARKA59	ARKA60	ARKA61	ARKA62	ARKA63	ARKA64	ARKA65	ARKA66	ARKA67	ARKA68	ARKA69	ARKA70	ARKA71	ARKA72	ARKA73	ARKA74	ARKA75	ARKA76	ARKA77	ARKA78	ARKA79	ARKA80	ARKA81	ARKA82	ARKA83	ARKA84	ARKA85	ARKA86	ARKA87	ARKA88	ARKA89	ARKA90	ARKA91	ARKA92	ARKA93	ARKA94	ARKA95	ARKA96	ARKA97	ARKA98	ARKA99	ARKA100	ARKA101	ARKA102	ARKA103	ARKA104	ARKA105	ARKA106	ARKA107	ARKA108	ARKA109	ARKA110	ARKA111	ARKA112	ARKA113	ARKA114	ARKA115	ARKA116	ARKA117	ARKA118	ARKA119	ARKA120	ARKA121	ARKA122	ARKA123	ARKA124	ARKA125	ARKA126	ARKA127	ARKA128	ARKA129	ARKA130	ARKA131	ARKA132	ARKA133	ARKA134	ARKA135	ARKA136	ARKA137	ARKA138	ARKA139	ARKA140	ARKA141	ARKA142	ARKA143	ARKA144	ARKA145	ARKA146	ARKA147	ARKA148	ARKA149	ARKA150	ARKA151	ARKA152	ARKA153	ARKA154	ARKA155	ARKA156	ARKA157	ARKA158	ARKA159	ARKA160	ARKA161	ARKA162	ARKA163	ARKA164	ARKA165	ARKA166	ARKA167	ARKA168	ARKA169	ARKA170	ARKA171	ARKA172	ARKA173	ARKA174	ARKA175	ARKA176	ARKA177	ARKA178	ARKA179	ARKA180	ARKA181	ARKA182	ARKA183	ARKA184	ARKA185	ARKA186	ARKA187	ARKA188	ARKA189	ARKA190	ARKA191	ARKA192	ARKA193	ARKA194	ARKA195	ARKA196	ARKA197	ARKA198	ARKA199	ARKA200	ARKA201	ARKA202	ARKA203	ARKA204	ARKA205	ARKA206	ARKA207	ARKA208	ARKA209	ARKA210	ARKA211	ARKA212	ARKA213	ARKA214	ARKA215	ARKA216	ARKA217	ARKA218	ARKA219	ARKA220	ARKA221	ARKA222	ARKA223	ARKA224	ARKA225	ARKA226	ARKA227	ARKA228	ARKA229	ARKA230	ARKA231	ARKA232	ARKA233	ARKA234	ARKA235	ARKA236	ARKA237	ARKA238	ARKA239	ARKA240	ARKA241	ARKA242	ARKA243	ARKA244	ARKA245	ARKA246	ARKA247	ARKA248	ARKA249	ARKA250	ARKA251	ARKA252	ARKA253	ARKA254	ARKA255	ARKA256	ARKA257	ARKA258	ARKA259	ARKA260	ARKA261	ARKA262	ARKA263	ARKA264	ARKA265	ARKA266	ARKA267	ARKA268	ARKA269	ARKA270	ARKA271	ARKA272	ARKA273	ARKA274	ARKA275	ARKA276	ARKA277	ARKA278	ARKA279	ARKA280	ARKA281	ARKA282	ARKA283	ARKA284	ARKA285	ARKA286	ARKA287	ARKA288	ARKA289	ARKA290	ARKA291	ARKA292	ARKA293	ARKA294	ARKA295	ARKA296	ARKA297	ARKA298	ARKA299	ARKA300	ARKA301	ARKA302	ARKA303	ARKA304	ARKA305	ARKA306	ARKA307	ARKA308	ARKA309	ARKA310	ARKA311	ARKA312	ARKA313	ARKA314	ARKA315	ARKA316	ARKA317	ARKA318	ARKA319	ARKA320	ARKA321	ARKA322	ARKA323	ARKA324	ARKA325	ARKA326	ARKA327	ARKA328	ARKA329	ARKA330	ARKA331	ARKA332	ARKA333	ARKA334	ARKA335	ARKA336	ARKA337	ARKA338	ARKA339	ARKA340	ARKA341	ARKA342	ARKA343	ARKA344	ARKA345	ARKA346	ARKA347	ARKA348	ARKA349	ARKA350	ARKA351	ARKA352	ARKA353	ARKA354	ARKA355	ARKA356	ARKA357	ARKA358	ARKA359	ARKA360	ARKA361	ARKA362	ARKA363	ARKA364	ARKA365	ARKA366	ARKA367	ARKA368	ARKA369	ARKA370	ARKA371	ARKA372	ARKA373	ARKA374	ARKA375	ARKA376	ARKA377	ARKA378	ARKA379	ARKA380	ARKA381	ARKA382	ARKA383	ARKA384	ARKA385	ARKA386	ARKA387	ARKA388	ARKA389	ARKA390	ARKA391	ARKA392	ARKA393	ARKA394	ARKA395	ARKA396	ARKA397	ARKA398	ARKA399	ARKA400	ARKA401	ARKA402	ARKA403	ARKA404	ARKA405	ARKA406	ARKA407	ARKA408	ARKA409	ARKA410	ARKA411	ARKA412	ARKA413	ARKA414	ARKA415	ARKA416	ARKA417	ARKA418	ARKA419	ARKA420	ARKA421	ARKA422	ARKA423	ARKA424	ARKA425	ARKA426	ARKA427	ARKA428	ARKA429	ARKA430	ARKA431	ARKA432	ARKA433	ARKA434	ARKA435	ARKA436	ARKA437	ARKA438	ARKA439	ARKA440	ARKA441	ARKA442	ARKA443	ARKA444	ARKA445	ARKA446	ARKA447	ARKA448	ARKA449	ARKA450	ARKA451	ARKA452	ARKA453	ARKA454	ARKA455	ARKA456	ARKA457	ARKA458	ARKA459	ARKA460	ARKA461	ARKA462	ARKA463	ARKA464	ARKA465	ARKA466	ARKA467	ARKA468	ARKA469	ARKA470	ARKA471	ARKA472	ARKA473	ARKA474	ARKA475	ARKA476	ARKA477	ARKA478	ARKA479	ARKA480	ARKA481	ARKA482	ARKA483	ARKA484	ARKA485	ARKA486	ARKA487	ARKA488	ARKA489	ARKA490	ARKA491	ARKA492	ARKA493	ARKA494	ARKA495	ARKA496	ARKA497	ARKA498	ARKA499	ARKA500	ARKA501	ARKA502	ARKA503	ARKA504	ARKA505	ARKA506	ARKA507	ARKA508	ARKA509	ARKA510	ARKA511	ARKA512	ARKA513	ARKA514	ARKA515	ARKA516	ARKA517	ARKA518	ARKA519	ARKA520	ARKA521	ARKA522	ARKA523	ARKA524	ARKA525	ARKA526	ARKA527	ARKA528	ARKA529	ARKA530	ARKA531	ARKA532	ARKA533	ARKA534	ARKA535	ARKA536	ARKA537	ARKA538	ARKA539	ARKA540	ARKA541	ARKA542	ARKA543	ARKA544	ARKA545	ARKA546	ARKA547	ARKA548	ARKA549	ARKA550	ARKA551	ARKA552	ARKA553	ARKA554	ARKA555	ARKA556	ARKA557	ARKA558	ARKA559	ARKA560	ARKA561	ARKA562	ARKA563	ARKA564	ARKA565	ARKA566	ARKA567	ARKA568	ARKA569	ARKA570	ARKA571	ARKA572	ARKA573	ARKA574	ARKA575	ARKA576	ARKA577	ARKA578	ARKA579	ARKA580	ARKA581	ARKA582	ARKA583	ARKA584	ARKA585	ARKA586	ARKA587	ARKA588	ARKA589	ARKA590	ARKA591	ARKA592	ARKA593	ARKA594	ARKA595	ARKA596	ARKA597	ARKA598	ARKA599	ARKA600	ARKA601	ARKA602	ARKA603	ARKA604	ARKA605	ARKA606	ARKA607	ARKA608	ARKA609	ARKA610	ARKA611	ARKA612	ARKA613	ARKA614	ARKA615	ARKA616	ARKA617	ARKA618	ARKA619	ARKA620	ARKA621	ARKA622	ARKA623	ARKA624	ARKA625	ARKA626	ARKA627	ARKA628	ARKA629	ARKA630	ARKA631	ARKA632	ARKA633	ARKA634	ARKA635	ARKA636	ARKA637	ARKA638	ARKA639	ARKA640	ARKA641	ARKA642	ARKA643	ARKA644	ARKA645	ARKA646	ARKA647	ARKA648	ARKA649	ARKA650	ARKA651	ARKA652	ARKA653	ARKA654	ARKA655	ARKA656	ARKA657	ARKA658	ARKA659	ARKA660	ARKA661	ARKA662	ARKA663	ARKA664	ARKA665	ARKA666	ARKA667	ARKA668	ARKA669	ARKA670	ARKA671	ARKA672	ARKA673	ARKA674	ARKA675	ARKA676	ARKA677	ARKA678	ARKA679	ARKA680	ARKA681	ARKA682	ARKA683	ARKA684	ARKA685	ARKA686	ARKA687	ARKA688	ARKA689	ARKA690	ARKA691	ARKA692	ARKA693	ARKA694	ARKA695	ARKA696	ARKA697	ARKA698	ARKA699	ARKA700	ARKA701	ARKA702	ARKA703	ARKA704	ARKA705	ARKA706	ARKA707	ARKA708	ARKA709	ARKA710	ARKA711	ARKA712	ARKA713	ARKA714	ARKA715	ARKA716	ARKA717	ARKA718	ARKA719	ARKA720	ARKA721	ARKA722	ARKA723	ARKA724	ARKA725	ARKA726	ARKA727	ARKA728	ARKA729	ARKA730	ARKA731	ARKA732	ARKA733	ARKA734	ARKA735	ARKA736	ARKA737	ARKA738	ARKA739	ARKA740	ARKA741	ARKA742	ARKA743	ARKA744	ARKA745	ARKA746	ARKA747	ARKA748	ARKA749	ARKA750	ARKA751	ARKA752	ARKA753	ARKA754	ARKA755	ARKA756	ARKA757	ARKA758	ARKA759	ARKA760	ARKA761	ARKA762	ARKA763	ARKA764	ARKA765	ARKA766	ARKA767	ARKA768	ARKA769	ARKA770	ARKA771	ARKA772	ARKA773	ARKA774	ARKA775	ARKA776	ARKA777	ARKA778	ARKA779	ARKA780	ARKA781	ARKA782	ARKA783	ARKA784	ARKA785	ARKA786	ARKA787	ARKA788	ARKA789	ARKA790	ARKA791	ARKA792	ARKA793	ARKA794	ARKA795	ARKA796	ARKA797	ARKA798	ARKA799	ARKA800	ARKA801	ARKA802	ARKA803	ARKA804	ARKA805	ARKA806	ARKA807	ARKA808	ARKA809	ARKA810	ARKA811	ARKA812	ARKA813	ARKA814	ARKA815	ARKA816	ARKA817	ARKA818	ARKA819	ARKA820	ARKA821	ARKA822	ARKA823	ARKA824	ARKA825	ARKA826	ARKA827	ARKA828	ARKA829	ARKA830	ARKA831	ARKA832	ARKA833	ARKA834	ARKA835	ARKA836	ARKA837	ARKA838	ARKA839	ARKA840	ARKA841	ARKA842	ARKA843	ARKA844	ARKA845	ARKA846	ARKA847	ARKA848	ARKA849	ARKA850	ARKA851	ARKA852	ARKA853	ARKA854	ARKA855	ARKA856	ARKA857	ARKA858	ARKA859	ARKA860	ARKA861	ARKA862	ARKA863	ARKA864	ARKA865	ARKA866	ARKA867	ARKA868	ARKA869	ARKA870	ARKA871	ARKA872	ARKA873	ARKA874	ARKA875	ARKA876	ARKA877	ARKA878	ARKA879	ARKA880	ARKA881	ARKA882	ARKA883	ARKA884	ARKA885	ARKA886	ARKA887	ARKA888	ARKA889	ARKA890	ARKA891	ARKA892	ARKA893	ARKA894	ARKA895	ARKA896	ARKA897	ARKA898	ARKA899	ARKA900	ARKA901	ARKA902	ARKA903	ARKA904	ARKA905	ARKA906	ARKA907	ARKA908	ARKA909	ARKA910	ARKA911	ARKA912	ARKA913	ARKA914	ARKA915	ARKA916	ARKA917	ARKA918	ARKA919	ARKA920	ARKA921	ARKA922	ARKA923	ARKA924	ARKA925	ARKA926	ARKA927	ARKA928	ARKA929	ARKA930	ARKA931	ARKA932	ARKA933	ARKA934	ARKA935	ARKA936	ARKA937	ARKA938	ARKA939	ARKA940	ARKA941	ARKA942	ARKA943	ARKA944	ARKA945	ARKA946	ARKA947	ARKA948	ARKA949	ARKA950	ARKA951	ARKA952	ARKA953	ARKA954	ARKA955	ARKA956	ARKA957	ARKA958	ARKA959	ARKA960	ARKA961	ARKA962	ARKA963	ARKA964	ARKA965	ARKA966	ARKA967	ARKA968	ARKA969	ARKA970	ARKA971	ARKA972	ARKA973	ARKA974	ARKA975	ARKA976	ARKA977	ARKA978	ARKA979	ARKA980	ARKA981	ARKA982	ARKA983	ARKA984	ARKA985	ARKA986	ARKA987	ARKA988	ARKA989	ARKA990	ARKA991	ARKA992	ARKA993	ARKA994	ARKA995	ARKA996	ARKA997	ARKA998	ARKA999	ARKA1000
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223



107117642 Muid Search on All Human Protein Sequences											
PCGENE	FILE NAME	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PROLIN	PROLIN	107117642									
PROK1	PROK1	107117642									
PROK2	PROK2	107117642									
PROK3	PROK3	107117642									
PROK4	PROK4	107117642									
PROK5	PROK5	107117642									
PROK6	PROK6	107117642									
PROK7	PROK7	107117642									
PROK8	PROK8	107117642									
PROK9	PROK9	107117642									
PROK10	PROK10	107117642									
PROK11	PROK11	107117642									
PROK12	PROK12	107117642									
PROK13	PROK13	107117642									
PROK14	PROK14	107117642									
PROK15	PROK15	107117642									
PROK16	PROK16	107117642									
PROK17	PROK17	107117642									
PROK18	PROK18	107117642									
PROK19	PROK19	107117642									
PROK20	PROK20	107117642									
PROK21	PROK21	107117642									
PROK22	PROK22	107117642									
PROK23	PROK23	107117642									
PROK24	PROK24	107117642									
PROK25	PROK25	107117642									
PROK26	PROK26	107117642									
PROK27	PROK27	107117642									
PROK28	PROK28	107117642									
PROK29	PROK29	107117642									
PROK30	PROK30	107117642									
PROK31	PROK31	107117642									
PROK32	PROK32	107117642									
PROK33	PROK33	107117642									
PROK34	PROK34	107117642									
PROK35	PROK35	107117642									
PROK36	PROK36	107117642									
PROK37	PROK37	107117642									
PROK38	PROK38	107117642									
PROK39	PROK39	107117642									
PROK40	PROK40	107117642									
PROK41	PROK41	107117642									
PROK42	PROK42	107117642									
PROK43	PROK43	107117642									
PROK44	PROK44	107117642									
PROK45	PROK45	107117642									
PROK46	PROK46	107117642									
PROK47	PROK47	107117642									
PROK48	PROK48	107117642									
PROK49	PROK49	107117642									
PROK50	PROK50	107117642									
PROK51	PROK51	107117642									
PROK52	PROK52	107117642									



225



PCGENE	197175cd Mafit Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
P100 HUMAN	60S RIBOSOMAL PROTEIN L3	142-192								
P101 HUMAN	60S RIBOSOMAL PROTEIN L3	18-163								
P102 HUMAN	60S RIBOSOMAL PROTEIN L3	192-235								
P103 HUMAN	53 KD RO PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (SS-A))	192-235								
P104 HUMAN	40 KD RO PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (SS-A))	192-235								
P105 HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C1C2 (HNRNP C1 AND HNRNP C2)	192-235								
P106 HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN L (HNRNP L)	192-235								
P107 HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN U	192-235								
P108 HUMAN	DNA-DIRECTED RNA POLYMERASE II 175 KD POLYPEPTIDE	192-235								
P109 HUMAN	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	192-235								
P110 HUMAN	DNA-DIRECTED RNA POLYMERASE II 135 KD POLYPEPTIDE	192-235								
P111 HUMAN	RETINOIC ACID RECEPTOR RXR-ALPHA	192-235								
P112 HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 1	192-235								
P113 HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 2	192-235								
P114 HUMAN	60S RIBOSOMAL PROTEIN S12	192-235								
P115 HUMAN	60S RIBOSOMAL PROTEIN S13	192-235								
P116 HUMAN	60S RIBOSOMAL PROTEIN S14	192-235								
P117 HUMAN	60S RIBOSOMAL PROTEIN S15	192-235								
P118 HUMAN	60S RIBOSOMAL PROTEIN S16	192-235								
P119 HUMAN	60S RIBOSOMAL PROTEIN S17	192-235								
P120 HUMAN	60S RIBOSOMAL PROTEIN S18	192-235								
P121 HUMAN	60S RIBOSOMAL PROTEIN S19	192-235								
P122 HUMAN	60S RIBOSOMAL PROTEIN S20	192-235								
P123 HUMAN	60S RIBOSOMAL PROTEIN S21	192-235								
P124 HUMAN	60S RIBOSOMAL PROTEIN S22	192-235								
P125 HUMAN	60S RIBOSOMAL PROTEIN S23	192-235								
P126 HUMAN	60S RIBOSOMAL PROTEIN S24	192-235								
P127 HUMAN	60S RIBOSOMAL PROTEIN S25	192-235								
P128 HUMAN	60S RIBOSOMAL PROTEIN S26	192-235								
P129 HUMAN	60S RIBOSOMAL PROTEIN S27	192-235								
P130 HUMAN	60S RIBOSOMAL PROTEIN S28	192-235								
P131 HUMAN	60S RIBOSOMAL PROTEIN S29	192-235								
P132 HUMAN	60S RIBOSOMAL PROTEIN S30	192-235								
P133 HUMAN	60S RIBOSOMAL PROTEIN S31	192-235								
P134 HUMAN	60S RIBOSOMAL PROTEIN S32	192-235								
P135 HUMAN	60S RIBOSOMAL PROTEIN S33	192-235								
P136 HUMAN	60S RIBOSOMAL PROTEIN S34	192-235								
P137 HUMAN	60S RIBOSOMAL PROTEIN S35	192-235								
P138 HUMAN	60S RIBOSOMAL PROTEIN S36	192-235								
P139 HUMAN	60S RIBOSOMAL PROTEIN S37	192-235								
P140 HUMAN	60S RIBOSOMAL PROTEIN S38	192-235								
P141 HUMAN	60S RIBOSOMAL PROTEIN S39	192-235								
P142 HUMAN	60S RIBOSOMAL PROTEIN S40	192-235								
P143 HUMAN	60S RIBOSOMAL PROTEIN S41	192-235								
P144 HUMAN	60S RIBOSOMAL PROTEIN S42	192-235								
P145 HUMAN	60S RIBOSOMAL PROTEIN S43	192-235								
P146 HUMAN	60S RIBOSOMAL PROTEIN S44	192-235								
P147 HUMAN	60S RIBOSOMAL PROTEIN S45	192-235								
P148 HUMAN	60S RIBOSOMAL PROTEIN S46	192-235								
P149 HUMAN	60S RIBOSOMAL PROTEIN S47	192-235								
P150 HUMAN	60S RIBOSOMAL PROTEIN S48	192-235								
P151 HUMAN	60S RIBOSOMAL PROTEIN S49	192-235								
P152 HUMAN	60S RIBOSOMAL PROTEIN S50	192-235								
P153 HUMAN	60S RIBOSOMAL PROTEIN S51	192-235								
P154 HUMAN	60S RIBOSOMAL PROTEIN S52	192-235								
P155 HUMAN	60S RIBOSOMAL PROTEIN S53	192-235								
P156 HUMAN	60S RIBOSOMAL PROTEIN S54	192-235								
P157 HUMAN	60S RIBOSOMAL PROTEIN S55	192-235								
P158 HUMAN	60S RIBOSOMAL PROTEIN S56	192-235								
P159 HUMAN	60S RIBOSOMAL PROTEIN S57	192-235								
P160 HUMAN	60S RIBOSOMAL PROTEIN S58	192-235								
P161 HUMAN	60S RIBOSOMAL PROTEIN S59	192-235								
P162 HUMAN	60S RIBOSOMAL PROTEIN S60	192-235								
P163 HUMAN	60S RIBOSOMAL PROTEIN S61	192-235								
P164 HUMAN	60S RIBOSOMAL PROTEIN S62	192-235								
P165 HUMAN	60S RIBOSOMAL PROTEIN S63	192-235								
P166 HUMAN	60S RIBOSOMAL PROTEIN S64	192-235								
P167 HUMAN	60S RIBOSOMAL PROTEIN S65	192-235								
P168 HUMAN	60S RIBOSOMAL PROTEIN S66	192-235								
P169 HUMAN	60S RIBOSOMAL PROTEIN S67	192-235								
P170 HUMAN	60S RIBOSOMAL PROTEIN S68	192-235								
P171 HUMAN	60S RIBOSOMAL PROTEIN S69	192-235								
P172 HUMAN	60S RIBOSOMAL PROTEIN S70	192-235								
P173 HUMAN	60S RIBOSOMAL PROTEIN S71	192-235								
P174 HUMAN	60S RIBOSOMAL PROTEIN S72	192-235								
P175 HUMAN	60S RIBOSOMAL PROTEIN S73	192-235								
P176 HUMAN	60S RIBOSOMAL PROTEIN S74	192-235								
P177 HUMAN	60S RIBOSOMAL PROTEIN S75	192-235								
P178 HUMAN	60S RIBOSOMAL PROTEIN S76	192-235								
P179 HUMAN	60S RIBOSOMAL PROTEIN S77	192-235								
P180 HUMAN	60S RIBOSOMAL PROTEIN S78	192-235								
P181 HUMAN	60S RIBOSOMAL PROTEIN S79	192-235								
P182 HUMAN	60S RIBOSOMAL PROTEIN S80	192-235								
P183 HUMAN	60S RIBOSOMAL PROTEIN S81	192-235								
P184 HUMAN	60S RIBOSOMAL PROTEIN S82	192-235								
P185 HUMAN	60S RIBOSOMAL PROTEIN S83	192-235								
P186 HUMAN	60S RIBOSOMAL PROTEIN S84	192-235								
P187 HUMAN	60S RIBOSOMAL PROTEIN S85	192-235								
P188 HUMAN	60S RIBOSOMAL PROTEIN S86	192-235								
P189 HUMAN	60S RIBOSOMAL PROTEIN S87	192-235								
P190 HUMAN	60S RIBOSOMAL PROTEIN S88	192-235								
P191 HUMAN	60S RIBOSOMAL PROTEIN S89	192-235								
P192 HUMAN	60S RIBOSOMAL PROTEIN S90	192-235								
P193 HUMAN	60S RIBOSOMAL PROTEIN S91	192-235								
P194 HUMAN	60S RIBOSOMAL PROTEIN S92	192-235								
P195 HUMAN	60S RIBOSOMAL PROTEIN S93	192-235								
P196 HUMAN	60S RIBOSOMAL PROTEIN S94	192-235								
P197 HUMAN	60S RIBOSOMAL PROTEIN S95	192-235								
P198 HUMAN	60S RIBOSOMAL PROTEIN S96	192-235								
P199 HUMAN	60S RIBOSOMAL PROTEIN S97	192-235								
P200 HUMAN	60S RIBOSOMAL PROTEIN S98	192-235								
P201 HUMAN	60S RIBOSOMAL PROTEIN S99	192-235								
P202 HUMAN	60S RIBOSOMAL PROTEIN S100	192-235								
P203 HUMAN	60S RIBOSOMAL PROTEIN S101	192-235								
P204 HUMAN	60S RIBOSOMAL PROTEIN S102	192-235								
P205 HUMAN	60S RIBOSOMAL PROTEIN S103	192-235								
P206 HUMAN	60S RIBOSOMAL PROTEIN S104	192-235								
P207 HUMAN	60S RIBOSOMAL PROTEIN S105	192-235								
P208 HUMAN	60S RIBOSOMAL PROTEIN S106	192-235								
P209 HUMAN	60S RIBOSOMAL PROTEIN S107	192-235								
P210 HUMAN	60S RIBOSOMAL PROTEIN S108	192-235								
P211 HUMAN	60S RIBOSOMAL PROTEIN S109	192-235								
P212 HUMAN	60S RIBOSOMAL PROTEIN S110	192-235								
P213 HUMAN	60S RIBOSOMAL PROTEIN S111	192-235								
P214 HUMAN	60S RIBOSOMAL PROTEIN S112	192-235								
P215 HUMAN	60S RIBOSOMAL PROTEIN S113	192-235								
P216 HUMAN	60S RIBOSOMAL PROTEIN S114	192-235								
P217 HUMAN	60S RIBOSOMAL PROTEIN S115	192-235								
P218 HUMAN	60S RIBOSOMAL PROTEIN S116	192-235								
P219 HUMAN	60S RIBOSOMAL PROTEIN S117	192-235								
P220 HUMAN	60S RIBOSOMAL PROTEIN S118	192-235								
P221 HUMAN	60S RIBOSOMAL PROTEIN S119	192-235								
P222 HUMAN	60S RIBOSOMAL PROTEIN S120	192-235								
P223 HUMAN	60S RIBOSOMAL PROTEIN S121	192-235								
P224 HUMAN	60S RIBOSOMAL PROTEIN S122	192-235								
P225 HUMAN	60S RIBOSOMAL PROTEIN S123	192-235								
P226 HUMAN	60S RIBOSOMAL PROTEIN S124	192-235								
P227 HUMAN	60S RIBOSOMAL PROTEIN S125	192-235								
P228 HUMAN	60S RIBOSOMAL PROTEIN S126	192-235								
P229 HUMAN	60S RIBOSOMAL PROTEIN S127	192-235								
P230 HUMAN	60S RIBOSOMAL PROTEIN S128	192-235								
P231 HUMAN	60S RIBOSOMAL PROTEIN S129	192-235								
P232 HUMAN	60S RIBOSOMAL PROTEIN S130	192-235								
P233 HUMAN	60S RIBOSOMAL PROTEIN S131	192-235								
P234 HUMAN	60S RIBOSOMAL PROTEIN S132	192-235								
P235 HUMAN	60S RIBOSOMAL PROTEIN S133	192-235								
P236 HUMAN	60S RIBOSOMAL PROTEIN S134	192-235								
P237 HUMAN	60S RIBOSOMAL PROTEIN S135	192-235								
P238 HUMAN	60S RIBOSOMAL PROTEIN S136	192-235								
P239 HUMAN	60S RIBOSOMAL PROTEIN S137	192-235								
P240 HUMAN	60S RIBOSOMAL PROTEIN S138	192-235								
P241 HUMAN	60S RIBOSOMAL PROTEIN S139	192-235								
P242 HUMAN	60S RIBOSOMAL PROTEIN S140	192-235								
P243 HUMAN	60S RIBOSOMAL PROTEIN S141	192-235								
P244 HUMAN	60S RIBOSOMAL PROTEIN S142	192-235								
P245 HUMAN	60S RIBOSOMAL PROTEIN S143	192-235								
P246 HUMAN	60S RIBOSOMAL PROTEIN S144	192-235								
P247 HUMAN	60S RIBOSOMAL PROTEIN S145	192-235								
P248 HUMAN	60S RIBOSOMAL PROTEIN S146	192-235								
P249 HUMAN	60S RIBOSOMAL PROTEIN S147	192-235								
P250 HUMAN	60S RIBOSOMAL PROTEIN S148	192-235								
P251 HUMAN	60S RIBOSOMAL PROTEIN S149	192-235		</						



PCGENE	10/1/95A Nuclei Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PTAB1 HUMAN	TRANSCRIPTION FACTOR RUN-B	296-323						
PTAB2 HUMAN	TRANSCRIPTION FACTOR RUN-B	291-313						
PTAB3 HUMAN	TRANSCRIPTION FACTOR RUN-D	278-305						
PTAB4 HUMAN	NUCLEOTIDE-ASSOCIATED PROTEIN TAU	211-228						
PTAB5 HUMAN	NUCLEOTIDE-ASSOCIATED PROTEIN TAU, FETAL	201-241						
PTAB6 HUMAN	TRANSCOBALANIN 1 PRECURSOR	330-353						
PTAB7 HUMAN	7-COMPLEX PROTEIN 1 (TCE-1)	316-340						
PTAB8 HUMAN	DNA NUCLEOTIDE-TRANSFERASE (EC 2.7.7.1) (TERMINAL ADDITION ENZYME)	61-95						
PTAB9 HUMAN	RECEPTOR TYROSINE KINASE TCR PRECURSOR (EC 2.7.1.12) (LIT-K-4)	644-678	1007-1036					
PTAB10 HUMAN	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)	135-162						
PTAB11 HUMAN	TRANSCRIPTION FACTOR E3 (FRAGMENT)	43-70	172-226					
PTAB12 HUMAN	TRANSCRIPTION ELONGATION FACTOR S-II	29-54						
PTAB13 HUMAN	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)	148-175						
PTAB14 HUMAN	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)	148-185						
PTAB15 HUMAN	TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2) (GHRHLAS1)	241-270						
PTAB16 HUMAN	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF)	87-114						
PTAB17 HUMAN	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE X (EC 2.3.2.13)	238-285						
PTAB18 HUMAN	TURBIDOSPONDIN PRECURSOR	110-163	384-314					
PTAB19 HUMAN	3-KETOACYL-CoA THIOLEASE PEROXISOMAL PRECURSOR (EC 2.3.1.16) (BETA-)	103-213						
PTAB20 HUMAN	PROTACTININ BETA PRECURSOR (CONTAINS SUBSTANCE P-NEUROKININ A)	11-38						
PTAB21 HUMAN	TRANSUCIN-LIKE ENHANCER PROTEIN 1	676-653						
PTAB22 HUMAN	TRANSUCIN-LIKE ENHANCER PROTEIN 2	94-123						
PTAB23 HUMAN	TRANSUCIN-LIKE ENHANCER PROTEIN 4 (FRAGMENT)	104-331						
PTAB24 HUMAN	DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3)	19-46	503-533					
PTAB25 HUMAN	DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3)	53-63						
PTAB26 HUMAN	TROPOMYOSIN, FIBROBLAST ISOFORM TM1	16-74	82-116					
PTAB27 HUMAN	TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE	16-43	47-74	191-237	243-277			
PTAB28 HUMAN	TROPOMYOSIN BETA CHAIN, SKELETAL MUSCLE	37-116	191-240					
PTAB29 HUMAN	TROPOMYOSIN ALPHA CHAIN, CARDIAC MUSCLE	16-74	82-116	191-237				
PTAB30 HUMAN	TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM10PL)	37-116	210-240	243-270				
PTAB31 HUMAN	TROPOMYOSIN, FIBROBLAST NON-MUSCLE TYPE (TM10NL)	46-80	111-138	158-196	207-234			
PTAB32 HUMAN	TROPOMYOSIN, CYTOSKELETAL TYPE (TM10NM)	46-80	111-138	172-199				
PTAB33 HUMAN	TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT)	35-59	147-178					
PTAB34 HUMAN	TRUPTIDYL-PEPTIDASE II (EC 3.4.14.10) (TPP III) (TRUPTIDYL)	153-187	1004-1031	1140-1187				
PTAB35 HUMAN	TPR ONCOGENE (FRAGMENT)	42-147						
PTAB36 HUMAN	THREB18 PROTEIN	18-45	242-269					
PTAB37 HUMAN	THYROTROPIN-RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBENIN)	144-383						
PTAB38 HUMAN	TROPOMYOSIN I, CARDIAC MUSCLE	36-63						
PTAB39 HUMAN	HIGH AFFINITY NEAVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	66-93	112-148					
PTAB40 HUMAN	TRANSFERIN RECEPTOR PROTEIN (TFR) (ANTIGEN CD31) (TF)	188-215	346-391					
PTAB41 HUMAN	THYROTROPIN RECEPTOR PRECURSOR (TSH-R)	83-117	428-447					
PTAB42 HUMAN	PROTEIN KINASE TKK (EC 2.7.1.1)	170-197	324-359	510-544	549-583			
PTAB43 HUMAN	NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK1 (EC 2.7.1.112)	150-177						
PTAB44 HUMAN	UBIQUITIN-ACTIVATING ENZYME E1 (A159 PROTEIN)	448-475						
PTAB45 HUMAN	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)	237-254						
PTAB46 HUMAN	UDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MICROSOAL (EC 2.4.1.17)	237-254						
PTAB47 HUMAN	RECEPTOR TYROSINE-PROTEIN KINASE UFO PRECURSOR (EC 2.7.1.112)	484-522						
PTAB48 HUMAN	UPSTREAM STIMULATORY FACTOR 1	331-395						
PTAB49 HUMAN	VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)	47-74	112-147					
PTAB50 HUMAN	VILIN	318-372	437-461	513-544				
PTAB51 HUMAN	VIMENTIN	119-146	233-260					
PTAB52 HUMAN	VINCULIN	95-134						
PTAB53 HUMAN	RETROVIRUS-RELATED PROTEASE (EC 3.4.23.1)	344-388						
PTAB54 HUMAN	WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112)	347-374						
PTAB55 HUMAN	WILMS TUMOR PROTEIN (WT1)	97-133						
PTAB56 HUMAN	X-BOX BINDING PROTEIN-1 (XBP-1) (TRES1 PROTEIN)							
PTAB57 HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)	180-211						
PTAB58 HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)	134-168	701-728					



PCGENE	1071754 Modl Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
P00C_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA PIGMENTOSUM)	364-291								
P00C_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)	81-110	1047-1081							
P00C_HUMAN	DNA-REPAIR PROTEIN XPC-H	37-57								
P00C_HUMAN	DNA-REPAIR PROTEIN XPD-H	79-56								
P00C_HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN K0X1) (FLAGMENT)	307-334	1071-1078		1407-1500	2013-2037	2146-2180			
P00C_HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENTIANCE R-)	17-62								
P00C_HUMAN	ZINC FINGER PROTEIN 41 (HRC1744) (FLAGMENT)	1-20	201-228							
P00C_HUMAN	ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP)	131-149								



**TABLE X**

**Search Results Summary for PCTLZIP,  
P1CTLZIP, and P2CTLZIP Motifs**



[illegible]



PHEMA MUMPM	133-148		PHEMA IADAN	231-237		PHEMA GYHOC	301-406
PHEMA MUMPR	133-148		PHEMA IABUD	234-260		PHEMA IAIIC	322-339
PHEMA MUMPS	133-148		PHEMA IACKA	234-260		PHEMA IABAN	306-323
PHEMA P11HW	348-360		PHEMA IACKO	231-247		PHEMA IABUD	320-337
PHEMA P12H	65-60		PHEMA IACKV	230-246		PHEMA IACKA	320-337
PHEMA P12HT	65-60		PHEMA IADA1	234-260		PHEMA IACKO	316-333
PHEMA RINDX	266-363		PHEMA IADA3	237-263		PHEMA IACKP	302-316
PHEMA BV6	7-84		PHEMA IADCE	234-260		PHEMA IACKO	302-316
PHEMA BV6CM	7-84		PHEMA IADH1	221-237		PHEMA IACKV	316-332
PHEMA BV6CLN	7-84		PHEMA IADH2	221-237		PHEMA IACKV	316-332
PVENY OHV11	42-57		PHEMA IADH3	221-237		PHEMA IADA1	320-337
PVP7 CAPYK	98-104		PHEMA IADH4	221-237		PHEMA IADCE	320-337
PVQ06 VACC0	22-67		PHEMA IADH6	221-237		PHEMA IADH1	306-323
PVQ01 BPP22	242-267		PHEMA IADH7	221-237		PHEMA IADH2	306-323
PVQ01 H8V8B	168-184		PHEMA IADM2	237-263		PHEMA IADH3	306-323
PVQ01 H3V11	210-228	317-332	PHEMA IADN2	234-260		PHEMA IADH4	306-323
PVQ08 BPT4	184-188		PHEMA IADN6	221-237		PHEMA IADH6	306-323
PVQ08 BPT4	686-800		PHEMA IADN7	237-263		PHEMA IADH7	306-323
PVQ08 H8V11	134-148		PHEMA IAFPR	230-246		PHEMA IADH2	322-339
PVQ10 BPPH2	183-198		PHEMA IAHAL	236-262		PHEMA IADH2	322-339
PVQ10 BPTZA	183-198		PHEMA IAHAR	236-261		PHEMA IADH3	322-339
PVQ10 H3V8A	109-124		PHEMA IAHCB	230-246		PHEMA IADH6	306-323
PVQ18 BPP1	81-90		PHEMA IAHCB	230-246		PHEMA IADH7	306-323
PVQ18 BPT4	468-483		PHEMA IAHCB	230-246		PHEMA IADH2	322-339
PVQ28 BPT4	97-112		PHEMA IAHDE	230-246		PHEMA IADH2	322-339
PVQ38 H3V11	20-36		PHEMA IAHFO	236-262		PHEMA IADH2	322-339
PVQ30 BPPH8	11-84		PHEMA IAHK6	236-262		PHEMA IADH2	322-339
PVQ38 BPOX2	22-37		PHEMA IAHK7	236-262		PHEMA IADH2	322-339
PVQ36 H8V8A	108-123		PHEMA IAHLE	230-246		PHEMA IADH2	322-339
PVQ37 BPT2	1263-1266		PHEMA IAHLO	230-246		PHEMA IADH2	322-339
PVQ37 H8V11	284-289		PHEMA IAHM1	236-262		PHEMA IADH2	322-339
PVQ85 H8V11	22-37	143-168	PHEMA IAHNM	236-262		PHEMA IADH2	322-339
PVQ86 H8V11	289-293		PHEMA IAHRO	236-262		PHEMA IADH2	322-339
PVQ86 H8V11	102-117		PHEMA IAHRA	236-262		PHEMA IADH2	322-339
PVQ89 H8V11	287-292		PHEMA IAHBP	230-246		PHEMA IADH2	322-339
PVQ86 H8V11	518-533		PHEMA IAHBW	230-246		PHEMA IADH2	322-339
PVQ8 BPPH2	234-248		PHEMA IAHTE	236-262		PHEMA IADH2	322-339
PVQ8 BPPH2	234-248		PHEMA IAHTO	236-262		PHEMA IADH2	322-339
PVQ8 BPPH2	67-72		PHEMA IAHUR	236-262		PHEMA IADH2	322-339
PVQ8 BPPH2	234-248		PHEMA IAHX	236-261		PHEMA IADH2	322-339
PVQ12 CV8F	264-278		PHEMA IAHLE	236-261		PHEMA IADH2	322-339
PVQ12 CV8L0	264-278		PHEMA IAHAA	233-240		PHEMA IADH2	322-339
PVQ12 CV8LY	264-278		PHEMA IAHAB	236-264		PHEMA IADH2	322-339
PVQ12 CV8M	264-278		PHEMA IAHAA	237-263		PHEMA IADH2	322-339
PVQ12 CV8Q	264-278		PHEMA IAHM1	237-263		PHEMA IADH2	322-339
PVQ12 CV8V	264-278		PHEMA IAHM2	237-263		PHEMA IADH2	322-339



PVQL2 CVRF3	442-467		PHEMA IAME9	221-237	231-247		PHEMA IANTO	321-338	
PVQL2 CVRFU	440-486	604-619	PHEMA IAMR	86-101			PHEMA IAHUR	321-338	
PVQL2 CVPR8	216-233		PHEMA IANT6	237-263			PHEMA IAJAP	317-334	
PVQL2 CVPRM	218-233		PHEMA IAGU7	221-237			PHEMA IAMAA	316-336	
PVQL2 IBV6	1066-1071		PHEMA IARUD	234-260			PHEMA IAMAB	324-341	
PVQL2 IBV8	1066-1070		PHEMA IABE2	234-260			PHEMA IAMAO	322-339	
PVQL2 IBVD2	1066-1071		PHEMA IASH2	234-260			PHEMA IAME1	322-339	
PVQL2 IBVK	1066-1070		PHEMA IASTA	230-246			PHEMA IAME2	322-339	
PVQL2 IBVM	1066-1070		PHEMA IATAI	235-261			PHEMA IAME6	306-323	
PVQL8 HSBVA	701-716		PHEMA IATKM	234-260			PHEMA IAMON	316-333	
PVQL8 PRVP	203-216		PHEMA IATKO	233-246			PHEMA IANT6	322-339	
PVQL8 HSBVC	476-490		PHEMA IATKR	230-246			PHEMA IAPUL	330-337	
PVQLC HSBV4	444-469		PHEMA IATRW	220-246			PHEMA IAGU7	306-323	
PVQLC HSBV8	437-442		PHEMA IAUDD	237-263			PHEMA IARUD	320-337	
PVQLC PRVIF	440-461		PHEMA IAU89	236-261			PHEMA IABE2	320-337	
PVQLD HSBV11	76-84		PHEMA IAV17	238-264			PHEMA IABH2	321-338	
PVQLD HSB2	76-84		PHEMA IAXUA	236-261			PHEMA IABTA	316-332	
PVQLF BRBVA	285-280		PHEMA IAZCO	237-263			PHEMA IATKM	320-337	380-397
PVQLF BRBVC	285-280		PHEMA IAZH2	221-237			PHEMA IAUDD	322-339	
PVQLF BRBVR	285-280		PHEMA IAZH3	221-237			PHEMA IAV17	322-339	
PVQLF HRSV1	285-280		PHEMA IAZUK	237-263			PHEMA IAZCO	322-339	
PVQLF HRSVA	285-280		PHEMA INBAA	116-131	286-310		PHEMA IAZH2	306-323	
PVQLF HRSVL	285-280		PHEMA INBBE	123-139	303-316		PHEMA IAZH3	306-323	
PVQLF HRSVR	285-280		PHEMA INBBO	116-132	293-308		PHEMA IAZUK	322-339	
PVQLF MUMPS	8-84		PHEMA INBFI	123-139	301-316		PHEMA MUMPM	101-118	
PVQLI VZVD	276-293		PHEMA INBFL	108-124	286-301		PHEMA MUMPR	101-118	
PVQLM HANTB	800-816		PHEMA INBGL	118-138	286-311		PHEMA NDVA	93-110	
PVQLM PTPV	743-768		PHEMA INBHK	116-132	293-308		PHEMA NDVB	93-110	
PVQLM SEOUR	801-816		PHEMA INBIB	108-124	286-303		PHEMA NDVD	93-110	
PVQLM SEOUS	800-816		PHEMA INBID	120-136	286-314		PHEMA NDVH	93-110	
PVQLY LABBQ	426-441		PHEMA INBLE	123-139	302-317		PHEMA NDVI	93-110	
PVQLY LABBJ	427-442		PHEMA INBMO	113-129	282-307		PHEMA NDVM	93-110	
PVQLY MOPEI	426-440		PHEMA INBME	118-132	286-311		PHEMA NDVQ	93-110	
PVMS3 REOVD	521-536		PHEMA INBNA	108-124	288-303		PHEMA NDVTO	93-110	
PVMS4 HPSB8	380-396		PHEMA INBOR	123-139	301-316		PHEMA NDVU	93-110	
PVMS4 HPSB9	187-202		PHEMA INBBI	123-139	301-316		PHEMA PHODV	36-63	
PVMS4 WHV1	378-393		PHEMA INBSJ	118-136	286-313		PHEMA P11HW	466-603	
PVMS4 WHV60	383-398		PHEMA INBSU	116-132	284-309		PHEMA P13H	111-128	
PVMS4 WHV7	383-398		PHEMA INBYI	116-132	286-311		PHEMA P13H4	111-128	
PVMS4 WHV8	383-398		PHEMA INBVK	123-139	303-318		PHEMA P13H5	111-128	
PVMS4 WHV81	383-398		PHEMA INBYB	108-124	286-301		PHEMA P13HT	111-128	
PVMS4 WHVW6	234-248		PHEMA MUMPM	133-148			PHEMA P13HU	111-128	
PVMT2 IANIN	26-40		PHEMA MUMPR	133-148			PHEMA P13HV	111-128	
PVMT2 IABAN	26-40		PHEMA MUMPS	133-148			PHEMA P13HW	111-128	
PVMT2 IAPW	26-40		PHEMA P11HW	346-360			PHEMA P13HX	111-128	
PVMT2 IAPR	26-40		PHEMA P13H	96-81			PHEMA P13H4	86-67	
PVMT2 IAPW	26-40		PHEMA P13HT	86-81					



PVMT2 IALE1	26-40	PHEMA P13B	324-340					PHEMA 8V41	86-102	
PVMT2 IALE2	26-40	PHEMA P13H4	324-340					PHEMA 8V5	84-101	
PVMT2 IAHAN	26-40	PHEMA P13HA	324-340					PHEMA 8V6CM	84-101	
PVMT2 IAPUE	26-40	PHEMA P13HT	324-340					PHEMA 8V6CP	84-101	
PVMT2 IABIN	26-40	PHEMA P13HU	324-340					PHEMA 8V6LN	84-101	
PVMT2 IAUDD	26-40	PHEMA P13HV	324-340					PVFO5 VACCC	280-297	
PVMT2 IAWIL	26-40	PHEMA P13HW	324-340					PVFO5 VACCP	280-297	
PVMT8 MYXVL	226-241	PHEMA P13HX	324-340					PVFO5 VACCV	281-288	
		PHEMA RINDK	306-383					PVFO5 VACCC	176-193	
		PHEMA 8V8	7-84					PVFO5 VACCV	176-193	
		PHEMA 8V6CM	7-84					PVQ27 HBVA	206-226	
		PHEMA 8V6CP	7-84					PVQ28 HBVI	173-190	
		PHEMA 8V6LN	7-84					PVQ35 HBVI	646-668	
		PVENV DRVH	42-57					PVQ43 HBVI	108-126	621-638
		PVENV EAV	28-41					PVQ67 HBVI	171-186	
		PVFT2 FOHPV	88-104					PVQ72 HBVI	1262-1268	
		PVFT7 CAPVK	88-104					PVQF1 HBVB	3073-3080	
		PVR05 VACCC	72-87					PVQL3 HBVB	1084-1111	
		PVQ01 HBVB	188-184					PVQLB HBVE1	736-763	
		PVQ01 HBVEB	208-225					PVQLB HBVE4	676-682	
		PVQ08 HBVI	134-148				317-332	PVQLB HBVEA	736-763	
		PVQ10 HBVA	108-124					PVQLB HBVEB	736-763	
		PVQ11 HBVI	103-118					PVQLB HBVEL	736-763	
		PVQ12 HBVI	270-286					PVQLB ILTV8	697-614	
		PVQ1 8PV1R	76-92					PVQLB ILTV8	607-624	
		PVQ28 HBVI	20-35					PVQLB ILTVT	607-624	
		PVQ66 BPOX2	22-37					PVQLC PRVF	180-187	
		PVQ36 HBVA	108-123					PVQLE VZVD	489-486	
		PVQ37 HBVI	284-288					PVOLF 8V5	401-418	
		PVQ41 HBVI	244-260					PVQLH HCMVA	385-382	
		PVQ46 HBVI	1244-1260					PVQLH HCMVT	384-381	
		PVQ55 HBVI	22-37				143-158	PVQLH HBVI1	246-262	803-820
		PVQ56 HBVI	285-283					PVQLH HBVI1	246-262	803-820
		PVQ58 HBVI	101-117					PVQLI HBVI1	43-80	
		PVQ59 HBVA	190-146				330-346	PVQLM BUNL7	61-98	
		PVQ65 HBVI	267-282					PVQLM BUNBH	61-98	
		PVQ68 HBVI	382-378				618-633	PVQLM PULNH	712-729	
		PVQ71 HBVA	88-105					PVQLM PUUMB	712-729	
		PVQ8 BPH2	234-240					PVQLM RVFV	344-361	
		PVQ8 BPZA	234-246					PVQLM RVFVZ	344-361	
		PVQ8 8PV1R	67-72					PVQLY LA98Q	12-84	
		PVQF1 HBVB	2210-2228					PVQLY LA88J	12-84	
		PVQL2 CV8P	123-139				174-180	PVQLY LYCVA	12-84	
		PVQL2 CV8L6	123-139				174-180	PVQLY LYCVW	12-84	
		PVQL2 CV8LY	123-139				174-190	PVQLY MOPEI	12-84	
		PVQL2 CV8M	123-138				174-180	PVMT REOVD	280-287	
		PVQL2 CV8Q	31-47				123-139	PVMT REOVL	280-287	



234



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PVMT2 IAFPR	28-40
PVMT2 IAFPW	28-40
PVMT2 IALES	28-40
PVMT2 IALES	28-40
PVMT2 IAMAN	28-40
PVMT2 IAPUE	28-40
PVMT2 IASIN	28-40
PVMT2 IAUDO	28-40
PVMT2 IAWIL	28-40
PVMT6 MYXVL	27B-2A1



## TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,  
P5CTLZIP, and P6CTLZIP Motifs



238



PVMO1 VACCV	183-101	128-144	PVQL2 CVM4	999-1018		PVENY THOOV	366-378		PHENA P12H	13-34	
PVM1 REOVD	227-246		PVQL2 CVM46	947-988		PVENY VACCC	288-318		PHENA P12HT	13-34	
PVM1 REOVL	227-246		PVQL2 CVM4H	968-877		PVQ01 VACCV	237-267		PHENA SV8	7-28	378-400
PVMAT HR8VA	44-62		PVQL2 CVF8H	84-83	1030-1067	PVQ01 VARV	288-318		PHENA SV6CM	7-28	378-400
PVMAT NDVA	180-208		PVQL2 CVP8U	84-83	1030-1066	PVQ06 VACCC	31-61		PHENA SV6CP	7-28	378-400
PVMAT NDVB	180-208		PVQL2 CVP8B	814-833		PVQ06 VARV	31-61		PHENA SV6LN	7-28	378-400
PVMP CAMVC	183-201		PVQL2 CVP8M	814-833		PVQ06 BPFF1	26-46		PVQ01 HSV8	188-180	
PVMP CAMVD	183-201		PVQL2 FIPV	1041-1060		PVQ12 HSV11	161-171		PVQ01 HSV8	188-180	
PVMP CAMVE	183-201		PVQL2 IBV8	688-807	771-780	PVQ22 HSV11	300-320		PVQ23 HSV11	688-810	
PVMP CAMVN	183-201		PVQL2 IBV8	688-808	770-780	PVQ38 HSV11	848-868		PVQ37 BPOX2	314-336	
PVMP CAMVS	183-201		PVQL2 IBVD2	688-807	771-780	PVQ51 HSV11	28-49		PVQ43 HSV11	167-178	
PVMP CAMVW	183-201		PVQL2 IBVK	687-808	770-780	PVQ63 HSV11	338-358		PVQ55 HSV11	288-309	
PVMP FHYD	180-188		PVQL2 IBVM	687-808	770-780	PVQ65 HSV11	117-137		PVQ56 HSV8A	85-108	
			PVQL8 HCMVA	708-726		PVQ74 HSV8A	124-144		PVQ58 HSV11	1155-1178	
			PVQL8 HCMVT	707-728		PVQL2 IBV8	328-348		PVQ58 HSV8A	206-287	
			PVQL8 HSB8U	117-138		PVQL2 IBV8	327-347		PVQ60 HSV11	30-61	
			PVQL8 ILTV8	268-276		PVQL2 IBVD2	328-348		PVQ63 HSV11	238-268	
			PVQL8 ILTVS	268-285		PVQL2 IBVD3	328-348		PVQ61 HSB8	186-1877	
			PVQL8 ILTVT	268-286		PVQL2 IBVK	327-347		PVQ63 HCMVA	167-178	
			PVQLC HSB11	3-94	467-488	PVQL2 IBVM	327-347	378-388	PVQL2 CVBF	128-1280	
			PVQLC HSB1K	3-94	467-488	PVQL2 IBVU2	310-330		PVQL2 CVBL8	128-1280	
			PVQLC HSBVC	475-494		PVQL8 EBV	732-752		PVQL2 CVBLV	128-1280	
			PVQLC CHAV	438-466		PVQLB HCMVA	750-770		PVQL2 CVBM	128-1280	
			PVQL8 RABVH	372-381		PVQLB HCMVT	761-771		PVQL2 CVBQ	128-1280	
			PVQL8 HSB8	44-83		PVQLB HSB23	78-88		PVQL2 CVBV	128-1280	
			PVQL1 VZVD	278-287		PVQLB HSB23	78-88		PVQL2 CVM4	1317-1338	
			PVQLM BUNGE	117-138		PVQLB HSB28	85-85		PVQL2 CVM45	1286-1288	
			PVQLM PHV	152-171		PVQLB HSB6U	72-82		PVQL2 CVMJH	1178-1197	
			PVQLM PTPV	887-1018		PVQLB HSB8A	83-83		PVQL8 HSB11	83-104	
			PVQLM PUUMH	155-174		PVQLB MCMV8	278-288		PVQL8 HSB1F	82-103	
			PVQLM PUUM5	155-174		PVQLF P13H4	738-758		PVQL8 HSB1K	82-103	
			PVQLM RVPV	830-848		PVQLF RABVE	283-303		PVQL8 HSB1P	83-104	
			PVQLM RVPV2	830-848		PVQL8 RABVH	454-474		PVQL8 MCMV3	136-160	
			PVQLM UUK	855-874		PVQL8 RABVP	454-474		PVQLC PRV8	448-487	
			PVQLY LYCVW	88-108		PVQL8 RABVP	454-474		PVQLF CDVO	335-367	
			PVQNB CMV	1185-1104		PVQL8 RABVT	454-474		PVQLF MEAB1	224-246	
			PVM3 REOVD	521-640		PVQL8 RABVT	454-474		PVQLF MEABY	224-246	
			PVME1 CVBM	171-180		PVQLM MCMV8	870-880		PVQLF MUMPM	224-246	
			PVME1 CVH22	136-156		PVQLM BUNL7	1328-1348		PVQLF MUMPM	448-487	
			PVME1 CVPF8	174-183		PVQLM BUNH	1328-1348		PVQLF MUMPM	448-487	
			PVME1 CVP8U	174-183		PVQLM BUNYH	888-1018		PVQLF MUMPM	448-487	
			PVME1 CVP8M	174-183		PVQLM HANTB	888-1018		PVQLF PHOVD	308-328	
			PVME1 CVTKE	171-180		PVQLM HANTH	1000-1020		PVQLF P11HC	468-477	
						PVQLM HANTL	1001-1021		PVQLF P12H	480-471	
						PVQLM HANTV	1001-1021		PVQLF P12H	480-471	
						PVQLM RVFVZ	1168-1178		PVQLF P12HT	480-471	
						PVQLM SEOUR	1000-1020		PVQLF P138	480-471	483-474



	PVGLM 8C0US	899-1018	PVOLF PLH4	463-474
	PVGLM UKK	926-945	PVOLF RINDX	220-261
	PVGLY LYCA	12-32	PVOLF RINDL	220-241
	PVGLY LYCVW	12-32	PVOLF BENDS	460-481
	PVGLY PIARV	12-32	PVOLF BENDE	460-481
	PVONB CPNV	141-161	PVOLF BENDH	460-481
	PVMAT MUMPS	310-330	PVOLF BENDJ	460-481
	PVMAT NDVA	308-329	PVOLF BENDZ	460-481
	PVMAT NDVB	308-329	PVOLF SV41	463-474
	PVMAT PIZHT	308-328	PVOLF SV8	446-467
	PVMAT PI4HA	312-332	PVOLH HCMVA	681-712
	PVMAT PI4HB	312-332	PVOLH HCMVT	680-711
	PVMAT SV41	308-328	PVOLH H8VE4	304-326
	PVMAT SV6	308-328	PVOLH H8VER	287-318
	PVME1 IBV6	74-94	PVOLH H8VSA	668-678
	PVME1 IBV8	74-94	PVOLI HSV2	2-23
	PVME1 IBV82	74-94	PVOLI HSV23	2-23
	PVME1 IBVK	74-94	PVOLM BUNGE	187-218
	PVMSA HPBD8	201-221	PVOLM BUNL7	180-211
	PVMSA HPB08	208-228	PVOLM BUNSH	180-211
	PVMSA HPBHE	283-313	PVOLM SUNYW	183-214
	PVMSA WHV1	207-227	PVGLY LABGQ	237-258
	PVMSA WHV69	212-232	PVGLY LABGJ	238-269
	PVMSA WHV7	212-232	PVQP8 EBV	87-88
	PVMSA WHV8	212-232	PVM01 VAGCC	281-302
	PVMSA WHV81	212-232	PVM01 VACCV	230-251
	PVMSA WHVW6	63-83	PVMAT HR8VA	189-190
			PVMAT RINDX	200-221
			PVMAT TRTV	123-143
			PVME1 CYNOC	64-85
			PVMSA HPBDB	201-222
			PVMSA HPBV0	70-91
			PVMSA HPBV2	244-266
			PVMSA HPBV4	244-265
			PVMSA HPBV6	244-268
			PVMSA HPBV8	233-284
			PVMSA HPBV0	70-91
			PVMSA HPBV1	233-264
			PVMSA HPBVJ	233-284
			PVMSA HPBVL	233-284
			PVMSA HPBVN	70-91
			PVMSA HPBV0	233-264
			PVMSA HPBPV	244-266
			PVMSA HPBVR	244-285
			PVMSA HPBV8	70-91"
			PVMSA HPBVW	233-254
			PVMSA HPBVY	233-254







## TABLE XII

Search Results Summary for P7CTLZIP,  
P8CTLZIP, and P9CTLZIP Motifs



PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE
PENV BAEVA	303-224	PENV FR3FV	380-403	PENV BLVAF	303-327		
PENV HV1B1	488-620	PENV2 FR3FV	380-403	PENV BLVAU	303-327		
PENV HV1B6	483-616	PENV BIV08	178-201	PENV BLVAV	303-327		
PENV HV1B8	484-616	PENV BIV27	202-230	PENV BLVB2	303-327		
PENV HV1B9	603-626	PENV FOAMV	864-887	PENV BLVB8	303-327		
PENV HV1EL	485-617	PENV HV123	176-188	PENV BLVJ	303-327		
PENV HV1H2	488-620	PENV HV28E	3-28	PENV FIVPE	781-805		
PENV HV1H3	488-620	PENV HV2CA	760-773	PENV FIVSD	778-803		
PENV HV1J3	610-632	PENV HV2D1	3-28	PENV FIVT2	780-804		
PENV HV1JR	480-612	PENV HV2G1	772-785	PHEMA CVBLY	381-415		
PENV HV1K8	604-626	PENV HV2NZ	777-800	PHEMA CVBM	381-416		
PENV HV1MA	600-622	PENV JSRV	641-664	PHEMA CVBQ	381-416		
PENV HV1MF	486-616	PENV 8FV1	884-887	PHEMA CVHOC	381-416		
PENV HV1ND	488-610	PENV 8FV3L	881-904	PHEMA INCCA	422-486		
PENV HV1PV	488-620	PENV 8IVM1	603-626	PHEMA INCEN	430-484		
PENV HV1R1	489-611	PENV 8IVM2	602-625	PHEMA INCOL	430-484		
PENV HV1Z2	123-146	PENV 8IVM3	601-624	PHEMA INCY	428-483		
PENV HV1Z6	487-616	PENV 8IVB4	606-629	PHEMA INCJH	443-487		
PENV HV1Z8	606-627	PENV 8IVSP	610-633	PHEMA INCKY	428-483		
PENV HV1ZM	488-620	PHEMA COVO	200-223	PHEMA INCM1	428-483		
PENV JSRV	376-388	PHEMA FIZH	66-88	PHEMA INGNA	428-483		
PENV MPBV	213-235	PHEMA FIZHT	66-88	PHEMA INCP1	430-484		
PENV SRV1	213-235	PVF11 VACCC	181-184	PHEMA INCP2	430-484		
PHEMA IAAIC	37-68	PVF16 VACCC	26-48	PHEMA INCP3	430-484		
PHEMA IABAN	21-43	PVF18 VACCP	3-28	PHEMA INCTA	430-484		
PHEMA IAD3	37-68	PVG11 AMEPV	313-338	PHEMA INCTA	430-484		
PHEMA IADH2	21-43	PVG28 H8V11	481-614	PHEMA MUMPM	101-126		
PHEMA IADH3	21-43	PVG43 H8V11	322-346	PHEMA MUMPR	101-126		
PHEMA IADH4	21-43	PVG52 H8V11	228-262	PHEMA MUMPS	101-126		
PHEMA IADH5	21-43	PVG67 H8V11	722-746	PHEMA PIHNV	28-63		
PHEMA IADH6	21-43	PVG12 CVBF	10-33	PENV BEV	82-98		
PHEMA IADH7	21-43	PVG13 CVBL9	681-674	PVF05 VACCC	280-304		
PHEMA IADH2	37-68	PVG12 CVBL9	10-33	PVF08 VACCP	280-304		
PHEMA IADMA	28-60	PVG12 CYM4	1287-1280	PVF08 VACCV	281-306		
PHEMA IADU3	37-68	PVG13 CYMA6	1216-1238	PVF08 VACCC	176-200		
PHEMA IAE6	21-43	PVG12 CYMAH	1126-1148	PVF08 VACCV	176-200		
PHEMA IAE7	37-68	PVG13 CVPF8	1274-1287	PVG01 VZVD	68-82		
PHEMA IAMAO	37-68	PVG13 CVPPU	1222-1285	PVG10 H8V8A	365-378		
PHEMA IAME1	37-68	PVG13 CVPR8	1060-1073	PVG12 H8V9A	68-82		
PHEMA IAME2	37-68	PVG12 CVPRM	1060-1073	PVG18 H8V11	88-112		
PHEMA IAME6	21-43	PVG13 FIV	1277-1300	PVG28 H8V11	172-187		
PHEMA IANT8	37-68	PVG12 H8V8	188-218	PVG43 H8V11	108-133		
PHEMA IAOU7	21-43	PVG13 H8V8	188-218	PVG87 H8V11	108-132		
PHEMA IATKM	33-66	PVG13 IBVD2	188-218	PVG72 H8V11	726-744		
PHEMA IAU00	37-68	PVG13 IBVD3	188-218	PVG1 IBVB	3801-3828		



244



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## TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF



247



248



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GENE	PROTEIN	AB Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500
PUL31	PROTEIN	AB Virus (No Bacteriophage)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				



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PGCENE	FILE NAME	FUNCTION	ADJ. Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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284



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286



AB Virus (No Bacteriophage)			AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
AB Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396</																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														



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Accession	Protein	Gene	Function	Host	Strain	Area 1	Area 2	Area 3	Area 4	Area 5	Area 6	Area 7	Area 8	Area 9	Area 10	Area 11	Area 12	Area 13	Area 14	Area 15	Area 16	Area 17	Area 18	Area 19	Area 20	Area 21	Area 22	Area 23	Area 24	Area 25	Area 26	Area 27	Area 28	Area 29	Area 30	Area 31	Area 32	Area 33	Area 34	Area 35	Area 36	Area 37	Area 38	Area 39	Area 40	Area 41	Area 42	Area 43	Area 44	Area 45	Area 46	Area 47	Area 48	Area 49	Area 50	Area 51	Area 52	Area 53	Area 54	Area 55	Area 56	Area 57	Area 58	Area 59	Area 60	Area 61	Area 62	Area 63	Area 64	Area 65	Area 66	Area 67	Area 68	Area 69	Area 70	Area 71	Area 72	Area 73	Area 74	Area 75	Area 76	Area 77	Area 78	Area 79	Area 80	Area 81	Area 82	Area 83	Area 84	Area 85	Area 86	Area 87	Area 88	Area 89	Area 90	Area 91	Area 92	Area 93	Area 94	Area 95	Area 96	Area 97	Area 98	Area 99	Area 100	Area 101	Area 102	Area 103	Area 104	Area 105	Area 106	Area 107	Area 108	Area 109	Area 110	Area 111	Area 112	Area 113	Area 114	Area 115	Area 116	Area 117	Area 118	Area 119	Area 120	Area 121	Area 122	Area 123	Area 124	Area 125	Area 126	Area 127	Area 128	Area 129	Area 130	Area 131	Area 132	Area 133	Area 134	Area 135	Area 136	Area 137	Area 138	Area 139	Area 140	Area 141	Area 142	Area 143	Area 144	Area 145	Area 146	Area 147	Area 148	Area 149	Area 150	Area 151	Area 152	Area 153	Area 154	Area 155	Area 156	Area 157	Area 158	Area 159	Area 160	Area 161	Area 162	Area 163	Area 164	Area 165	Area 166	Area 167	Area 168	Area 169	Area 170	Area 171	Area 172	Area 173	Area 174	Area 175	Area 176	Area 177	Area 178	Area 179	Area 180	Area 181	Area 182	Area 183	Area 184	Area 185	Area 186	Area 187	Area 188	Area 189	Area 190	Area 191	Area 192	Area 193	Area 194	Area 195	Area 196	Area 197	Area 198	Area 199	Area 200	Area 201	Area 202	Area 203	Area 204	Area 205	Area 206	Area 207	Area 208	Area 209	Area 210	Area 211	Area 212	Area 213	Area 214	Area 215	Area 216	Area 217	Area 218	Area 219	Area 220	Area 221	Area 222	Area 223	Area 224	Area 225	Area 226	Area 227	Area 228	Area 229	Area 230	Area 231	Area 232	Area 233	Area 234	Area 235	Area 236	Area 237	Area 238	Area 239	Area 240	Area 241	Area 242	Area 243	Area 244	Area 245	Area 246	Area 247	Area 248	Area 249	Area 250	Area 251	Area 252	Area 253	Area 254	Area 255	Area 256	Area 257	Area 258	Area 259	Area 260	Area 261	Area 262	Area 263	Area 264	Area 265	Area 266	Area 267	Area 268	Area 269	Area 270	Area 271	Area 272	Area 273	Area 274	Area 275	Area 276	Area 277	Area 278	Area 279	Area 280	Area 281	Area 282	Area 283	Area 284	Area 285	Area 286	Area 287	Area 288	Area 289	Area 290	Area 291	Area 292	Area 293	Area 294	Area 295	Area 296	Area 297	Area 298	Area 299	Area 300	Area 301	Area 302	Area 303	Area 304	Area 305	Area 306	Area 307	Area 308	Area 309	Area 310	Area 311	Area 312	Area 313	Area 314	Area 315	Area 316	Area 317	Area 318	Area 319	Area 320	Area 321	Area 322	Area 323	Area 324	Area 325	Area 326	Area 327	Area 328	Area 329	Area 330	Area 331	Area 332	Area 333	Area 334	Area 335	Area 336	Area 337	Area 338	Area 339	Area 340	Area 341	Area 342	Area 343	Area 344	Area 345	Area 346	Area 347	Area 348	Area 349	Area 350	Area 351	Area 352	Area 353	Area 354	Area 355	Area 356	Area 357	Area 358	Area 359	Area 360	Area 361	Area 362	Area 363	Area 364	Area 365	Area 366	Area 367	Area 368	Area 369	Area 370	Area 371	Area 372	Area 373	Area 374	Area 375	Area 376	Area 377	Area 378	Area 379	Area 380	Area 381	Area 382	Area 383	Area 384	Area 385	Area 386	Area 387	Area 388	Area 389	Area 390	Area 391	Area 392	Area 393	Area 394	Area 395	Area 396	Area 397	Area 398	Area 399	Area 400	Area 401	Area 402	Area 403	Area 404	Area 405	Area 406	Area 407	Area 408	Area 409	Area 410	Area 411	Area 412	Area 413	Area 414	Area 415	Area 416	Area 417	Area 418	Area 419	Area 420	Area 421	Area 422	Area 423	Area 424	Area 425	Area 426	Area 427	Area 428	Area 429	Area 430	Area 431	Area 432	Area 433	Area 434	Area 435	Area 436	Area 437	Area 438	Area 439	Area 440	Area 441	Area 442	Area 443	Area 444	Area 445	Area 446	Area 447	Area 448	Area 449	Area 450	Area 451	Area 452	Area 453	Area 454	Area 455	Area 456	Area 457	Area 458	Area 459	Area 460	Area 461	Area 462	Area 463	Area 464	Area 465	Area 466	Area 467	Area 468	Area 469	Area 470	Area 471	Area 472	Area 473	Area 474	Area 475	Area 476	Area 477	Area 478	Area 479	Area 480	Area 481	Area 482	Area 483	Area 484	Area 485	Area 486	Area 487	Area 488	Area 489	Area 490	Area 491	Area 492	Area 493	Area 494	Area 495	Area 496	Area 497	Area 498	Area 499	Area 500	Area 501	Area 502	Area 503	Area 504	Area 505	Area 506	Area 507	Area 508	Area 509	Area 510	Area 511	Area 512	Area 513	Area 514	Area 515	Area 516	Area 517	Area 518	Area 519	Area 520	Area 521	Area 522	Area 523	Area 524	Area 525	Area 526	Area 527	Area 528	Area 529	Area 530	Area 531	Area 532	Area 533	Area 534	Area 535	Area 536	Area 537	Area 538	Area 539	Area 540	Area 541	Area 542	Area 543	Area 544	Area 545	Area 546	Area 547	Area 548	Area 549	Area 550	Area 551	Area 552	Area 553	Area 554	Area 555	Area 556	Area 557	Area 558	Area 559	Area 560	Area 561	Area 562	Area 563	Area 564	Area 565	Area 566	Area 567	Area 568	Area 569	Area 570	Area 571	Area 572	Area 573	Area 574	Area 575	Area 576	Area 577	Area 578	Area 579	Area 580	Area 581	Area 582	Area 583	Area 584	Area 585	Area 586	Area 587	Area 588	Area 589	Area 590	Area 591	Area 592	Area 593	Area 594	Area 595	Area 596	Area 597	Area 598	Area 599	Area 600	Area 601	Area 602	Area 603	Area 604	Area 605	Area 606	Area 607	Area 608	Area 609	Area 610	Area 611	Area 612	Area 613	Area 614	Area 615	Area 616	Area 617	Area 618	Area 619	Area 620	Area 621	Area 622	Area 623	Area 624	Area 625	Area 626	Area 627	Area 628	Area 629	Area 630	Area 631	Area 632	Area 633	Area 634	Area 635	Area 636	Area 637	Area 638	Area 639	Area 640	Area 641	Area 642	Area 643	Area 644	Area 645	Area 646	Area 647	Area 648	Area 649	Area 650	Area 651	Area 652	Area 653	Area 654	Area 655	Area 656	Area 657	Area 658	Area 659	Area 660	Area 661	Area 662	Area 663	Area 664	Area 665	Area 666	Area 667	Area 668	Area 669	Area 670	Area 671	Area 672	Area 673	Area 674	Area 675	Area 676	Area 677	Area 678	Area 679	Area 680	Area 681	Area 682	Area 683	Area 684	Area 685	Area 686	Area 687	Area 688	Area 689	Area 690	Area 691	Area 692	Area 693	Area 694	Area 695	Area 696	Area 697	Area 698	Area 699	Area 700	Area 701	Area 702	Area 703	Area 704	Area 705	Area 706	Area 707	Area 708	Area 709	Area 710	Area 711	Area 712	Area 713	Area 714	Area 715	Area 716	Area 717	Area 718	Area 719	Area 720	Area 721	Area 722	Area 723	Area 724	Area 725	Area 726	Area 727	Area 728	Area 729	Area 730	Area 731	Area 732	Area 733	Area 734	Area 735	Area 736	Area 737	Area 738	Area 739	Area 740	Area 741	Area 742	Area 743	Area 744	Area 745	Area 746	Area 747	Area 748	Area 749	Area 750	Area 751	Area 752	Area 753	Area 754	Area 755	Area 756	Area 757	Area 758	Area 759	Area 760	Area 761	Area 762	Area 763	Area 764	Area 765	Area 766	Area 767	Area 768	Area 769	Area 770	Area 771	Area 772	Area 773	Area 774	Area 775	Area 776	Area 777	Area 778	Area 779	Area 780	Area 781	Area 782	Area 783	Area 784	Area 785	Area 786	Area 787	Area 788	Area 789	Area 790	Area 791	Area 792	Area 793	Area 794	Area 795	Area 796	Area 797	Area 798	Area 799	Area 800	Area 801	Area 802	Area 803	Area 804	Area 805	Area 806	Area 807	Area 808	Area 809	Area 810	Area 811	Area 812	Area 813	Area 814	Area 815	Area 816	Area 817	Area 818	Area 819	Area 820	Area 821	Area 822	Area 823	Area 824	Area 825	Area 826	Area 827	Area 828	Area 829	Area 830	Area 831	Area 832	Area 833	Area 834	Area 835	Area 836	Area 837	Area 838	Area 839	Area 840	Area 841	Area 842	Area 843	Area 844	Area 845	Area 846	Area 847	Area 848	Area 849	Area 850	Area 851	Area 852	Area 853	Area 854	Area 855	Area 856	Area 857	Area 858	Area 859	Area 860	Area 861	Area 862	Area 863	Area 864	Area 865	Area 866	Area 867	Area 868	Area 869	Area 870	Area 871	Area 872	Area 873	Area 874	Area 875	Area 876	Area 877	Area 878	Area 879	Area 880	Area 881	Area 882	Area 883	Area 884	Area 885	Area 886	Area 887	Area 888	Area 889	Area 890	Area 891	Area 892	Area 893	Area 894	Area 895	Area 896	Area 897	Area 898	Area 899	Area 900	Area 901	Area 902	Area 903	Area 904	Area 905	Area 906	Area 907	Area 908	Area 909	Area 910	Area 911	Area 912	Area 913	Area 914	Area 915	Area 916	Area 917	Area 918	Area 919	Area 920	Area 921	Area 922	Area 923	Area 924	Area 925	Area 926	Area 927	Area 928	Area 929	Area 930	Area 931	Area 932	Area 933	Area 934	Area 935	Area 936	Area 937	Area 938	Area 939	Area 940	Area 941	Area 942	Area 943	Area 944	Area 945	Area 946	Area 947	Area 948	Area 949	Area 950	Area 951	Area 952	Area 953	Area 954	Area 955	Area 956	Area 957	Area 958	Area 959	Area 960	Area 961	Area 962	Area 963	Area 964	Area 965	Area 966	Area 967	Area 968	Area 969	Area 970	Area 971	Area 972	Area 973	Area 974	Area 975	Area 976	Area 977	Area 978	Area 979	Area 980	Area 981	Area 982	Area 983	Area 984	Area 985	Area 986	Area 987	Area 988	Area 989	Area 990	Area 991	Area 992	Area 993	Area 994	Area 995	Area 996	Area 997	Area 998	Area 999	Area 1000
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292



[illegible]



294



ACCESSION	FUNCTION	ALL VIRUSES (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	104-221								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	164-182								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	92-113								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	103-401								
OROTA PSEUDOTOGATA MULTICAPSID POLYOMYXOVIRUS (OP)	OROTA PSEUDOTOGATA MULTICAPSID POLYOMYXOVIRUS (OP)	133-153								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-99	100-156							
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	11-40	51-48							
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	28-46								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	4-38								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-54								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	18-35								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	5-26	16-52							
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	22-38	44-44							
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-18	22-38							
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-47								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-42								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	109-137								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	54-70								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	150-166								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	54-80								
CHLORIS STRIATE MOSAIC VIRUS	CHLORIS STRIATE MOSAIC VIRUS	100-135	141-162							
SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	56-73								
HUMAN ADENOVIRUS TYPE 7	HUMAN ADENOVIRUS TYPE 7	103-188								
BEST NECTROTIC YELLOW VEIN MOSAIC VIRUS (ISOLATE P2)	BEST NECTROTIC YELLOW VEIN MOSAIC VIRUS (ISOLATE P2)	90-108								
OUTGRAVIA CALIFORNICA NUCLEAR POLYOMYXOVIRUS	OUTGRAVIA CALIFORNICA NUCLEAR POLYOMYXOVIRUS	65-90								
SOYBEAN CHLOROTIC MOTTLE VIRUS	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-142								
SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	31-44								
SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	31-54								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-54								
MEASLES VIRUS (STRAIN HALLS)	MEASLES VIRUS (STRAIN HALLS)	96-128								
SOYBEAN CHLOROTIC MOTTLE VIRUS	SOYBEAN CHLOROTIC MOTTLE VIRUS	100-103								
SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	100-27	153-173	541-561	617-613	764-784				
SOYBEAN CHLOROTIC MOTTLE VIRUS	SOYBEAN CHLOROTIC MOTTLE VIRUS	54-77								
HUMAN ADENOVIRUS TYPE 7	HUMAN ADENOVIRUS TYPE 7	16-41	63-77							
SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	205-220								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	354-374								
FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	104-121								
FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	48-47								
FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	64-100								
FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	114-134	134-169							
FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	FOWLPOX VIRUS (ISOLATE HP-23HIMUNICH)	113-128								
SQUAN FOAMY VIRUS (TYPE 37 STRAIN LX1)	SQUAN FOAMY VIRUS (TYPE 37 STRAIN LX1)	32-78								
HUMAN SPINARETROVIRUS	HUMAN SPINARETROVIRUS	208-210								
HERPESVIRUS SAMRIN (SUBGROUP C / STRAIN 481)	HERPESVIRUS SAMRIN (SUBGROUP C / STRAIN 481)	64-90								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	205-222								
MADEIRA DISEASE HERPESVIRUS (STRAIN BC-1)	MADEIRA DISEASE HERPESVIRUS (STRAIN BC-1)	175-190								
MADEIRA DISEASE HERPESVIRUS (STRAIN AD3)	MADEIRA DISEASE HERPESVIRUS (STRAIN AD3)	101-121								
HUMAN CYTOMEGALOVIRUS (STRAIN AD164)	HUMAN CYTOMEGALOVIRUS (STRAIN AD164)	64-102								
VACCINIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	141-156								
MURINE CORONAVIRUS MCV	MURINE CORONAVIRUS MCV	141-156								
MURINE CORONAVIRUS MCV	MURINE CORONAVIRUS MCV	7-33								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	61-90								
HUMAN ADENOVIRUS TYPE 41	HUMAN ADENOVIRUS TYPE 41	51-73								
EPSTEIN-BARR VIRUS (STRAIN D91-B)	EPSTEIN-BARR VIRUS (STRAIN D91-B)	76-100	128-155	211-241	330-346					
SQUANTUM INDESCENT VIRUS (INSECT INDESCENT VIRUS TYPE 22)	SQUANTUM INDESCENT VIRUS (INSECT INDESCENT VIRUS TYPE 22)	21-46								



296



**TABLE XIV**

**SEARCH RESULTS SUMMARY**

**FOR P23TLZIPC MOTIF**



298



299



ECG	FILE NAME	PROTEIN	PK-TYPE	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PPH 1	PPH 1	STRUCTURAL POLYPROTEIN	PPH 1	121-316					
PPH 2	PPH 2	STRUCTURAL POLYPROTEIN	PPH 2	121-317					
PPH 3	PPH 3	STRUCTURAL POLYPROTEIN	PPH 3	121-318					
PPH 4	PPH 4	STRUCTURAL POLYPROTEIN	PPH 4	121-319					
PPH 5	PPH 5	STRUCTURAL POLYPROTEIN	PPH 5	121-320					
PPH 6	PPH 6	STRUCTURAL POLYPROTEIN	PPH 6	121-321					
PPH 7	PPH 7	STRUCTURAL POLYPROTEIN	PPH 7	121-322					
PPH 8	PPH 8	STRUCTURAL POLYPROTEIN	PPH 8	121-323					
PPH 9	PPH 9	STRUCTURAL POLYPROTEIN	PPH 9	121-324					
PPH 10	PPH 10	STRUCTURAL POLYPROTEIN	PPH 10	121-325					
PPH 11	PPH 11	STRUCTURAL POLYPROTEIN	PPH 11	121-326					
PPH 12	PPH 12	STRUCTURAL POLYPROTEIN	PPH 12	121-327					
PPH 13	PPH 13	STRUCTURAL POLYPROTEIN	PPH 13	121-328					
PPH 14	PPH 14	STRUCTURAL POLYPROTEIN	PPH 14	121-329					
PPH 15	PPH 15	STRUCTURAL POLYPROTEIN	PPH 15	121-330					
PPH 16	PPH 16	STRUCTURAL POLYPROTEIN	PPH 16	121-331					
PPH 17	PPH 17	STRUCTURAL POLYPROTEIN	PPH 17	121-332					
PPH 18	PPH 18	STRUCTURAL POLYPROTEIN	PPH 18	121-333					
PPH 19	PPH 19	STRUCTURAL POLYPROTEIN	PPH 19	121-334					
PPH 20	PPH 20	STRUCTURAL POLYPROTEIN	PPH 20	121-335					
PPH 21	PPH 21	STRUCTURAL POLYPROTEIN	PPH 21	121-336					
PPH 22	PPH 22	STRUCTURAL POLYPROTEIN	PPH 22	121-337					
PPH 23	PPH 23	STRUCTURAL POLYPROTEIN	PPH 23	121-338					
PPH 24	PPH 24	STRUCTURAL POLYPROTEIN	PPH 24	121-339					
PPH 25	PPH 25	STRUCTURAL POLYPROTEIN	PPH 25	121-340					
PPH 26	PPH 26	STRUCTURAL POLYPROTEIN	PPH 26	121-341					
PPH 27	PPH 27	STRUCTURAL POLYPROTEIN	PPH 27	121-342					
PPH 28	PPH 28	STRUCTURAL POLYPROTEIN	PPH 28	121-343					
PPH 29	PPH 29	STRUCTURAL POLYPROTEIN	PPH 29	121-344					
PPH 30	PPH 30	STRUCTURAL POLYPROTEIN	PPH 30	121-345					
PPH 31	PPH 31	STRUCTURAL POLYPROTEIN	PPH 31	121-346					
PPH 32	PPH 32	STRUCTURAL POLYPROTEIN	PPH 32	121-347					
PPH 33	PPH 33	STRUCTURAL POLYPROTEIN	PPH 33	121-348					
PPH 34	PPH 34	STRUCTURAL POLYPROTEIN	PPH 34	121-349					
PPH 35	PPH 35	STRUCTURAL POLYPROTEIN	PPH 35	121-350					
PPH 36	PPH 36	STRUCTURAL POLYPROTEIN	PPH 36	121-351					
PPH 37	PPH 37	STRUCTURAL POLYPROTEIN	PPH 37	121-352					
PPH 38	PPH 38	STRUCTURAL POLYPROTEIN	PPH 38	121-353					
PPH 39	PPH 39	STRUCTURAL POLYPROTEIN	PPH 39	121-354					
PPH 40	PPH 40	STRUCTURAL POLYPROTEIN	PPH 40	121-355					
PPH 41	PPH 41	STRUCTURAL POLYPROTEIN	PPH 41	121-356					
PPH 42	PPH 42	STRUCTURAL POLYPROTEIN	PPH 42	121-357					
PPH 43	PPH 43	STRUCTURAL POLYPROTEIN	PPH 43	121-358					
PPH 44	PPH 44	STRUCTURAL POLYPROTEIN	PPH 44	121-359					
PPH 45	PPH 45	STRUCTURAL POLYPROTEIN	PPH 45	121-360					
PPH 46	PPH 46	STRUCTURAL POLYPROTEIN	PPH 46	121-361					
PPH 47	PPH 47	STRUCTURAL POLYPROTEIN	PPH 47	121-362					
PPH 48	PPH 48	STRUCTURAL POLYPROTEIN	PPH 48	121-363					
PPH 49	PPH 49	STRUCTURAL POLYPROTEIN	PPH 49	121-364					
PPH 50	PPH 50	STRUCTURAL POLYPROTEIN	PPH 50	121-365					
PPH 51	PPH 51	STRUCTURAL POLYPROTEIN	PPH 51	121-366					
PPH 52	PPH 52	STRUCTURAL POLYPROTEIN	PPH 52	121-367					
PPH 53	PPH 53	STRUCTURAL POLYPROTEIN	PPH 53	121-368					
PPH 54	PPH 54	STRUCTURAL POLYPROTEIN	PPH 54	121-369					
PPH 55	PPH 55	STRUCTURAL POLYPROTEIN	PPH 55	121-370					
PPH 56	PPH 56	STRUCTURAL POLYPROTEIN	PPH 56	121-371					
PPH 57	PPH 57	STRUCTURAL POLYPROTEIN	PPH 57	121-372					
PPH 58	PPH 58	STRUCTURAL POLYPROTEIN	PPH 58	121-373					
PPH 59	PPH 59	STRUCTURAL POLYPROTEIN	PPH 59	121-374					
PPH 60	PPH 60	STRUCTURAL POLYPROTEIN	PPH 60	121-375					
PPH 61	PPH 61	STRUCTURAL POLYPROTEIN	PPH 61	121-376					
PPH 62	PPH 62	STRUCTURAL POLYPROTEIN	PPH 62	121-377					
PPH 63	PPH 63	STRUCTURAL POLYPROTEIN	PPH 63	121-378					
PPH 64	PPH 64	STRUCTURAL POLYPROTEIN	PPH 64	121-379					
PPH 65	PPH 65	STRUCTURAL POLYPROTEIN	PPH 65	121-380					
PPH 66	PPH 66	STRUCTURAL POLYPROTEIN	PPH 66	121-381					
PPH 67	PPH 67	STRUCTURAL POLYPROTEIN	PPH 67	121-382					
PPH 68	PPH 68	STRUCTURAL POLYPROTEIN	PPH 68	121-383					
PPH 69	PPH 69	STRUCTURAL POLYPROTEIN	PPH 69	121-384					
PPH 70	PPH 70	STRUCTURAL POLYPROTEIN	PPH 70	121-385					
PPH 71	PPH 71	STRUCTURAL POLYPROTEIN	PPH 71	121-386					
PPH 72	PPH 72	STRUCTURAL POLYPROTEIN	PPH 72	121-387					
PPH 73	PPH 73	STRUCTURAL POLYPROTEIN	PPH 73	121-388					
PPH 74	PPH 74	STRUCTURAL POLYPROTEIN	PPH 74	121-389					
PPH 75	PPH 75	STRUCTURAL POLYPROTEIN	PPH 75	121-390					
PPH 76	PPH 76	STRUCTURAL POLYPROTEIN	PPH 76	121-391					
PPH 77	PPH 77	STRUCTURAL POLYPROTEIN	PPH 77	121-392					
PPH 78	PPH 78	STRUCTURAL POLYPROTEIN	PPH 78	121-393					
PPH 79	PPH 79	STRUCTURAL POLYPROTEIN	PPH 79	121-394					
PPH 80	PPH 80	STRUCTURAL POLYPROTEIN	PPH 80	121-395					
PPH 81	PPH 81	STRUCTURAL POLYPROTEIN	PPH 81	121-396					
PPH 82	PPH 82	STRUCTURAL POLYPROTEIN	PPH 82	121-397					
PPH 83	PPH 83	STRUCTURAL POLYPROTEIN	PPH 83	121-398					
PPH 84	PPH 84	STRUCTURAL POLYPROTEIN	PPH 84	121-399					
PPH 85	PPH 85	STRUCTURAL POLYPROTEIN	PPH 85	121-400					
PPH 86	PPH 86	STRUCTURAL POLYPROTEIN	PPH 86	121-401					
PPH 87	PPH 87	STRUCTURAL POLYPROTEIN	PPH 87	121-402					
PPH 88	PPH 88	STRUCTURAL POLYPROTEIN	PPH 88	121-403					
PPH 89	PPH 89	STRUCTURAL POLYPROTEIN	PPH 89	121-404					
PPH 90	PPH 90	STRUCTURAL POLYPROTEIN	PPH 90	121-405					
PPH 91	PPH 91	STRUCTURAL POLYPROTEIN	PPH 91	121-406					
PPH 92	PPH 92	STRUCTURAL POLYPROTEIN	PPH 92	121-407					
PPH 93	PPH 93	STRUCTURAL POLYPROTEIN	PPH 93	121-408					
PPH 94	PPH 94	STRUCTURAL POLYPROTEIN	PPH 94	121-409					
PPH 95	PPH 95	STRUCTURAL POLYPROTEIN	PPH 95	121-410					
PPH 96	PPH 96	STRUCTURAL POLYPROTEIN	PPH 96	121-411					
PPH 97	PPH 97	STRUCTURAL POLYPROTEIN	PPH 97	121-412					
PPH 98	PPH 98	STRUCTURAL POLYPROTEIN	PPH 98	121-413					
PPH 99	PPH 99	STRUCTURAL POLYPROTEIN	PPH 99	121-414					
PPH 100	PPH 100	STRUCTURAL POLYPROTEIN	PPH 100	121-415					



GENE NAME	FUNCTION	AP Virus (see description page 2)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PRP1	PROTEIN	PRP1	11-109						
PRP2	PROTEIN	PRP2	11-109						
PRP3	PROTEIN	PRP3	11-109						
PRP4	PROTEIN	PRP4	11-109						
PRP5	PROTEIN	PRP5	11-109						
PRP6	PROTEIN	PRP6	11-109						
PRP7	PROTEIN	PRP7	11-109						
PRP8	PROTEIN	PRP8	11-109						
PRP9	PROTEIN	PRP9	11-109						
PRP10	PROTEIN	PRP10	11-109						
PRP11	PROTEIN	PRP11	11-109						
PRP12	PROTEIN	PRP12	11-109						
PRP13	PROTEIN	PRP13	11-109						
PRP14	PROTEIN	PRP14	11-109						
PRP15	PROTEIN	PRP15	11-109						
PRP16	PROTEIN	PRP16	11-109						
PRP17	PROTEIN	PRP17	11-109						
PRP18	PROTEIN	PRP18	11-109						
PRP19	PROTEIN	PRP19	11-109						
PRP20	PROTEIN	PRP20	11-109						
PRP21	PROTEIN	PRP21	11-109						
PRP22	PROTEIN	PRP22	11-109						
PRP23	PROTEIN	PRP23	11-109						
PRP24	PROTEIN	PRP24	11-109						
PRP25	PROTEIN	PRP25	11-109						
PRP26	PROTEIN	PRP26	11-109						
PRP27	PROTEIN	PRP27	11-109						
PRP28	PROTEIN	PRP28	11-109						
PRP29	PROTEIN	PRP29	11-109						
PRP30	PROTEIN	PRP30	11-109						
PRP31	PROTEIN	PRP31	11-109						
PRP32	PROTEIN	PRP32	11-109						
PRP33	PROTEIN	PRP33	11-109						
PRP34	PROTEIN	PRP34	11-109						
PRP35	PROTEIN	PRP35	11-109						
PRP36	PROTEIN	PRP36	11-109						
PRP37	PROTEIN	PRP37	11-109						
PRP38	PROTEIN	PRP38	11-109						
PRP39	PROTEIN	PRP39	11-109						
PRP40	PROTEIN	PRP40	11-109						
PRP41	PROTEIN	PRP41	11-109						
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PRP43	PROTEIN	PRP43	11-109						
PRP44	PROTEIN	PRP44	11-109						
PRP45	PROTEIN	PRP45	11-109						
PRP46	PROTEIN	PRP46	11-109						
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PRP93	PROTEIN	PRP93	11-109						
PRP94	PROTEIN	PRP94	11-109						
PRP95	PROTEIN	PRP95	11-109						
PRP96	PROTEIN	PRP96	11-109						
PRP97	PROTEIN	PRP97	11-109						
PRP98	PROTEIN	PRP98	11-109						
PRP99	PROTEIN	PRP99	11-109						
PRP100	PROTEIN	PRP100	11-109						



302



[illegible]



304



305



PROTEIN	FUNCTION	PROTEIN	FUNCTION	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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FUNCTION	PROTEIN	ALL Viruses (no bacteriophages)	AREA1 38-59	AREA2 38-111	AREA3 38-111	AREA4 38-111	AREA5 38-111	AREA6 38-111	AREA7 38-111	AREA8 38-111	AREA9 38-111	AREA10 38-111	AREA11 38-111	AREA12 38-111	AREA13 38-111	AREA14 38-111	AREA15 38-111	AREA16 38-111	AREA17 38-111	AREA18 38-111	AREA19 38-111	AREA20 38-111	AREA21 38-111	AREA22 38-111	AREA23 38-111	AREA24 38-111	AREA25 38-111	AREA26 38-111	AREA27 38-111	AREA28 38-111	AREA29 38-111	AREA30 38-111	AREA31 38-111	AREA32 38-111	AREA33 38-111	AREA34 38-111	AREA35 38-111	AREA36 38-111	AREA37 38-111	AREA38 38-111	AREA39 38-111	AREA40 38-111	AREA41 38-111	AREA42 38-111	AREA43 38-111	AREA44 38-111	AREA45 38-111	AREA46 38-111	AREA47 38-111	AREA48 38-111	AREA49 38-111	AREA50 38-111	AREA51 38-111	AREA52 38-111	AREA53 38-111	AREA54 38-111	AREA55 38-111	AREA56 38-111	AREA57 38-111	AREA58 38-111	AREA59 38-111	AREA60 38-111	AREA61 38-111	AREA62 38-111	AREA63 38-111	AREA64 38-111	AREA65 38-111	AREA66 38-111	AREA67 38-111	AREA68 38-111	AREA69 38-111	AREA70 38-111	AREA71 38-111	AREA72 38-111	AREA73 38-111	AREA74 38-111	AREA75 38-111	AREA76 38-111	AREA77 38-111	AREA78 38-111	AREA79 38-111	AREA80 38-111	AREA81 38-111	AREA82 38-111	AREA83 38-111	AREA84 38-111	AREA85 38-111	AREA86 38-111	AREA87 38-111	AREA88 38-111	AREA89 38-111	AREA90 38-111	AREA91 38-111	AREA92 38-111	AREA93 38-111	AREA94 38-111	AREA95 38-111	AREA96 38-111	AREA97 38-111	AREA98 38-111	AREA99 38-111	AREA100 38-111	AREA101 38-111	AREA102 38-111	AREA103 38-111	AREA104 38-111	AREA105 38-111	AREA106 38-111	AREA107 38-111	AREA108 38-111	AREA109 38-111	AREA110 38-111	AREA111 38-111	AREA112 38-111	AREA113 38-111	AREA114 38-111	AREA115 38-111	AREA116 38-111	AREA117 38-111	AREA118 38-111	AREA119 38-111	AREA120 38-111	AREA121 38-111	AREA122 38-111	AREA123 38-111	AREA124 38-111	AREA125 38-111	AREA126 38-111	AREA127 38-111	AREA128 38-111	AREA129 38-111	AREA130 38-111	AREA131 38-111	AREA132 38-111	AREA133 38-111	AREA134 38-111	AREA135 38-111	AREA136 38-111	AREA137 38-111	AREA138 38-111	AREA139 38-111	AREA140 38-111	AREA141 38-111	AREA142 38-111	AREA143 38-111	AREA144 38-111	AREA145 38-111	AREA146 38-111	AREA147 38-111	AREA148 38-111	AREA149 38-111	AREA150 38-111	AREA151 38-111	AREA152 38-111	AREA153 38-111	AREA154 38-111	AREA155 38-111	AREA156 38-111	AREA157 38-111	AREA158 38-111	AREA159 38-111	AREA160 38-111	AREA161 38-111	AREA162 38-111	AREA163 38-111	AREA164 38-111	AREA165 38-111	AREA166 38-111	AREA167 38-111	AREA168 38-111	AREA169 38-111	AREA170 38-111	AREA171 38-111	AREA172 38-111	AREA173 38-111	AREA174 38-111	AREA175 38-111	AREA176 38-111	AREA177 38-111	AREA178 38-111	AREA179 38-111	AREA180 38-111	AREA181 38-111	AREA182 38-111	AREA183 38-111	AREA184 38-111	AREA185 38-111	AREA186 38-111	AREA187 38-111	AREA188 38-111	AREA189 38-111	AREA190 38-111	AREA191 38-111	AREA192 38-111	AREA193 38-111	AREA194 38-111	AREA195 38-111	AREA196 38-111	AREA197 38-111	AREA198 38-111	AREA199 38-111	AREA200 38-111	AREA201 38-111	AREA202 38-111	AREA203 38-111	AREA204 38-111	AREA205 38-111	AREA206 38-111	AREA207 38-111	AREA208 38-111	AREA209 38-111	AREA210 38-111	AREA211 38-111	AREA212 38-111	AREA213 38-111	AREA214 38-111	AREA215 38-111	AREA216 38-111	AREA217 38-111	AREA218 38-111	AREA219 38-111	AREA220 38-111	AREA221 38-111	AREA222 38-111	AREA223 38-111	AREA224 38-111	AREA225 38-111	AREA226 38-111	AREA227 38-111	AREA228 38-111	AREA229 38-111	AREA230 38-111	AREA231 38-111	AREA232 38-111	AREA233 38-111	AREA234 38-111	AREA235 38-111	AREA236 38-111	AREA237 38-111	AREA238 38-111	AREA239 38-111	AREA240 38-111	AREA241 38-111	AREA242 38-111	AREA243 38-111	AREA244 38-111	AREA245 38-111
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TABLE XV  
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSV-Z
5	X-YTSVI-Z
	X-YTSVIT-Z
	X-YTSVITI-Z
	X-YTSVITIE-Z
	X-YTSVITIEL-Z
	X-YTSVITIELS-Z
	X-YTSVITIELSN-Z
10	X-YTSVITIELSNI-Z
	X-YTSVITIELSNIK-Z
	X-YTSVITIELSNIKE-Z
	X-YTSVITIELSNIKEN-Z
	X-YTSVITIELSNIKENK-Z
	X-YTSVITIELSNIKENKC-Z
	X-YTSVITIELSNIKENKCN-Z
	X-YTSVITIELSNIKENKCNG-Z
15	X-YTSVITIELSNIKENKCNGT-Z
	X-YTSVITIELSNIKENKCNGTD-Z
	X-YTSVITIELSNIKENKCNGTDA-Z
	X-YTSVITIELSNIKENKCNGTDAK-Z
	X-YTSVITIELSNIKENKCNGTDAKV-Z
	X-YTSVITIELSNIKENKCNGTDAKVK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKL-Z
20	X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z
25	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z
30	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

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The ne lett r amin acid code is used.



Additi nally,

"X" may r present an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butylloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amide group; a T-butylloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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**TABLE XVI**  
**RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG**  
**AMINO TRUNCATIONS**

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
	X-AVTELQLLMQST-Z
10	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
	X-ELDKYKNAVTELQLLMQST-Z
15	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,



"x" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or t-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"z" may represent a carboxyl group; an amide group; a t-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDF-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

- 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier



group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVIII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
	X-QVNEKINQSLAFIRKSDELL-Z
15	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-DPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-YDPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE XIX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
CARBOXY TRUNCATIONS

X-ITL-Z  
 X-ITLN-Z  
 X-ITLNN-Z  
 5 X-ITLNN-S-Z  
 X-ITLNN-SV-Z  
 X-ITLNN-SVA-Z  
 X-ITLNN-SVAL-Z  
 X-ITLNN-SVALD-Z  
 X-ITLNN-SVALDP-Z  
 X-ITLNN-SVALDPI-Z  
 10 X-ITLNN-SVALDPID-Z  
 X-ITLNN-SVALDPIDI-Z  
 X-ITLNN-SVALDPIDIS-Z  
 X-ITLNN-SVALDPIDISI-Z  
 X-ITLNN-SVALDPIDISIE-Z  
 X-ITLNN-SVALDPIDISIEL-Z  
 X-ITLNN-SVALDPIDISIELN-Z  
 X-ITLNN-SVALDPIDISIELNK-Z  
 15 X-ITLNN-SVALDPIDISIELNKA-Z  
 X-ITLNN-SVALDPIDISIELNKAK-Z  
 X-ITLNN-SVALDPIDISIELNKAKS-Z  
 X-ITLNN-SVALDPIDISIELNKAKSD-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDL-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLE-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEE-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEES-Z  
 20 X-ITLNN-SVALDPIDISIELNKAKSDLEESK-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKE-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEW-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWI-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWIR-Z  
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.



TABLE XX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25	X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.



TABLE XXI  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
CARBOXY TRUNCATIONS

X-ALG-Z  
 X-ALGV-Z  
 X-ALGVA-Z  
 5 X-ALGVAT-Z  
 X-ALGVATS-Z  
 X-ALGVATSA-Z  
 X-ALGVATSAQ-Z  
 X-ALGVATSAQI-Z  
 X-ALGVATSAQIT-Z  
 X-ALGVATSAQITA-Z  
 10 X-ALGVATSAQITAA-Z  
 X-ALGVATSAQITA-AV-Z  
 X-ALGVATSAQITA-AVA-Z  
 X-ALGVATSAQITA-AVAL-Z  
 X-ALGVATSAQITA-AVALV-Z  
 X-ALGVATSAQITA-AVALVE-Z  
 X-ALGVATSAQITA-AVALVEA-Z  
 X-ALGVATSAQITA-AVALVEAK-Z  
 15 X-ALGVATSAQITA-AVALVEAKQ-Z  
 X-ALGVATSAQITA-AVALVEAKQA-Z  
 X-ALGVATSAQITA-AVALVEAKQAR-Z  
 X-ALGVATSAQITA-AVALVEAKQARS-Z  
 X-ALGVATSAQITA-AVALVEAKQARSD-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIE-Z  
 20 X-ALGVATSAQITA-AVALVEAKQARSDIEK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKL-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKE-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEA-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XXII  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE XXIII  
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- 5 X-TSVITIELSNIKENKCNCTDAKVKLIKQELDKYKN-Z  
X-SVITIELSNIKENKCNCTDAKVKLIKQELDKYKNA-Z  
X-VITIELSNIKENKCNCTDAKVKLIKQELDKYKNAV-Z  
X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSV-Z  
X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSVL-Z  
X-VSKVLHLEGEVNKIALSTNKAVVSLSNGVSVL-Z  
X-SKVLHLEGEVNKIALSTNKAVVSLSNGVSVLT-Z  
X-KVLHLEGEVNKIALSTNKAVVSLSNGVSVLTS-Z  
X-LEGEVNKIALSTNKAVVSLSNGVSVLTSKVLD-Z  
10 X-GEVNKIALSTNKAVVSLSNGVSVLTSKVLDLK-Z  
X-EVNKIALSTNKAVVSLSNGVSVLTSKVLDLKN-Z  
X-VNKIALSTNKAVVSLSNGVSVLTSKVLDLKNY-Z  
X-NKIALSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z  
X-KIALSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z  
X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSV-Z  
15 X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSV-Z  
X-VSKVLHLEGEVNKIALSTNKAVVSLSNGVSVL-Z  
X-SKVLHLEGEVNKIALSTNKAVVSLSNGVSVLT-Z  
X-KVLHLEGEVNKIALSTNKAVVSLSNGVSVLTS-Z  
X-LEGEVNKIALSTNKAVVSLSNGVSVLTSKVLD-Z  
X-GEVNKIALSTNKAVVSLSNGVSVLTSKVLDLK-Z  
X-EVNKIALSTNKAVVSLSNGVSVLTSKVLDLKN-Z  
20 X-VNKIALSTNKAVVSLSNGVSVLTSKVLDLKNY-Z  
X-NKIALSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z  
X-KIALSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAQSDLEESKEWIRRSN-Z  
X-LNNSVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z  
X-NNSVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z  
X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z  
X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z  
X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSI-Z  
X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIG-Z  
30 X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGN-Z  
X-PIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNW-Z  
X-IDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWH-Z  
X-DISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQ-Z  
X-ISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQS-Z  
X-SIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSS-Z  
X-IELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSST-Z  
35 X-ELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSSTT-Z  
X-TAAVALVEAKQARSQIEKLKEAIRDITNKAVQSVQS-Z



X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z  
 X-LVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z  
 X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLI-Z  
 X-EAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIV-Z  
 X-AKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVA-Z  
 X-KQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAI-Z  
 X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIAIK-Z  
 5 X-ARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIAIKS-Z  
 X-RSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIAIKSV-Z  
 X-SDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIAIKSVQ-Z  
 X-KLKEAIRDTNKAVQSVQSSIGNLIVAIAIKSVQDYVN-Z  
 X-LKEAIRDTNKAVQSVQSSIGNLIVAIAIKSVQDYVNK-Z  
 X-AIRDTNKAVQSVQSSIGNLIVAIAIKSVQDYVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWKRVDFLEENITALLEEAIQQEKNMYELQK-Z  
 X-QEWKRVDFLEENITALLEEAIQQEKNMYELQKL-Z  
 X-EWVKRVDFLEENITALLEEAIQQEKNMYELQKLN-Z  
 X-WKRVDFLEENITALLEEAIQQEKNMYELQKLNS-Z  
 X-ERKRVDFLEENITALLEEAIQQEKNMYELQKLNSW-Z  
 X-RKRVDFLEENITALLEEAIQQEKNMYELQKLNSWD-Z  
 15 X-KRVDFLEENITALLEEAIQQEKNMYELQKLNSWDV-Z  
 X-VDFLEENITALLEEAIQQEKNMYELQKLNSWDVF-Z  
 X-DFLEENITALLEEAIQQEKNMYELQKLNSWDVFG-Z  
 X-FLEENITALLEEAIQQEKNMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDLGPPISLERLDVGTNLGNIAIAKLEAKELL-Z  
 X-HRIDLGPPISLERLDVGTNLGNIAIAKLEAKELLE-Z  
 X-RIDLGPPISLERLDVGTNLGNIAIAKLEAKELLES-Z  
 X-IDLGPPISLERLDVGTNLGNIAIAKLEAKELLESS-Z  
 X-DLGPPISLERLDVGTNLGNIAIAKLEAKELLESSD-Z  
 X-LGPPISLERLDVGTNLGNIAIAKLEAKELLESSDQ-Z  
 X-GPPISLERLDVGTNLGNIAIAKLEAKELLESSDQI-Z  
 25 X-PPISLERLDVGTNLGNIAIAKLEAKELLESSDQIL-Z  
 X-PISLERLDVGTNLGNIAIAKLEAKELLESSDQILR-Z  
 X-SLERLDVGTNLGNIAIAKLEAKELLESSDQILRSM-Z  
 X-LERLDVGTNLGNIAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

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"Z" may represent a carb xyl group; an amido group; a T-butyloxycarbonyl group; a macr molecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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#### 5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, *et al.*, 1989, *Molecular Cloning, A Laboratory Manual*, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butylloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,



above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the  
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may  
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to  
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

### 30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,

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bel w, and assays for antiviral activity are described in Section 5.5.2, bel w.

#### 5.5.1 ASSAYS FOR CELL FUSION EVENTS

5 Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

10 Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus  
15 that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each  
20 peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used.  
25 After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as  
30 crystal violet stain, may be used to facilitate the visualization of syncytial formation.

#### 5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides  
35 of the invention may be measured, for example, by



asily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4<sup>+</sup> cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4<sup>+</sup> cells by cell-free HIV. Such an assay may compris culturing an appropriate



concentration (i.e., TCID<sub>50</sub>) of virus and CD-4<sup>+</sup> cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.



Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of  $10^4$  to  $10^5$  pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

#### 5.6. USES OF THE PEPTIDES OF THE INVENTION

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral



structure with a cell membrane. Among the intracellular disorders involving coiled coil peptide structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5 With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10 These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not  
15 limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

20 Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B  
25 viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses  
30 and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides  
35 form non-covalent protein-protein interactions which



are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4<sup>+</sup> cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific



peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

#### 5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for  
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the  
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,  
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially  
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-  
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic  
35 compounds, natural products, and other sources of



potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, 5 for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 10 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

15 In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time 20 sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide, 25 thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

30 (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and 35



(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that



complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or  
5 indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or  
10 DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored  
15 complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

20 Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107  
25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

30 The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two  
35 peptides to interact and bind, thus forming a complex.



In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have



been formed. The various formats are described briefly below.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.



Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41Δ178 peptides and by assaying test



compunds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion  
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter  
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room  
15 temperature for one hour, unbound DP-178 and test compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d  
20 is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be conducted. Test compounds showing an ability to  
disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to  
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand or inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a  
35 solid support such as a microtiter well. DP178



binding to M41Δ178 is then quantitated by measuring the fraction of DP178 that is bound as <sup>125</sup>I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to  
5 M41Δ178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

10

#### 5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.  
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may  
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal,  
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline  
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration  
35 of the peptides of the invention or other inhibitory



agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adenovirus-associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure



to an HIV virus. Examples of such prophylactic use of these peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with



little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the  $IC_{50}$  (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable adjuvant in order to enhance the immunological



r sponse. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydr xide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest



will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above  
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the  
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be  
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,  
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective  
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these  
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated  
35



for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be



add d, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)



is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

## 6.1. MATERIALS AND METHODS

### 6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H<sub>2</sub>O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15 $\mu$  spherical) with a linear gradient; H<sub>2</sub>O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

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### 6.1.2. VIRUS

The HIV-1<sub>LA1</sub> virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2µm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of serial diluted virus was added to 75µl AA5 cells at a concentration of  $2 \times 10^5$ /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID<sub>50</sub> was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). The titer of the HIV-1<sub>LA1</sub> and HIV-1<sub>MN</sub> stocks used for these studies, as measured on the AA5 cell line, was approximately  $1.4 \times 10^6$  and  $3.8 \times 10^4$  TCID<sub>50</sub>/ml, respectively.

### 6.1.3. CELL FUSION ASSAY

Approximately  $7 \times 10^4$  Molt cells were incubated with  $1 \times 10^4$  CEM cells chronically infected with the HIV-1<sub>LA1</sub> virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100µl culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10µl and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated giant cells were estimated by microscopic examination



at a 40x magnification which allowed visualization of the entire well in a single field.

#### 6.1.4. CELL FREE VIRUS INFECTION ASSAY

Synthetic peptides were incubated at 37°C with  
5 either 247 TCID<sub>50</sub> (for experiment depicted in FIG. 2),  
or 62 TCID<sub>50</sub> (for experiment depicted in FIG.3) units  
of HIV-1<sub>LAI</sub> virus or 25 TCID<sub>50</sub> units of HIV-2<sub>MBZ</sub> and CEM  
CD4<sup>+</sup> cells at peptide concentrations of 0, 0.04, 0.4,  
10 4.0, and 40µg/ml for 7 days. The resulting reverse  
transcriptase (RT) activity in counts per minute was  
determined using the assay described, below, in  
Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J.  
Hyg. 27: 493-497 for an explanation of TCID<sub>50</sub>  
calculations.

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#### 6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was  
adapted from Goff et al. (Goff, S. et al., 1981, J.  
Virol. 38:239-248) and Willey et al. (Willey, R. et  
20 al., 1988, J. Virol. 62:139-147). Supernatants from  
virus/cell cultures are adjusted to 1% Triton-X100. A  
10µl sample of supernatant was added to 50µl of RT  
cocktail in a 96-well U-bottom microtitre plate and  
the samples incubated at 37°C for 90 min. The RT  
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM  
MgCl<sub>2</sub>, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01),  
0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-  
01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-  
radioactive dTTP, and 10µCi/ml <sup>32</sup>P-dTTP (Amersham, cat.  
30 No. PB.10167).

After the incubation period, 40µl of reaction  
mixture was applied to a Schleicher and Schuell (S+S)  
NA45 membrane (or DE81 paper) saturated in 2 x SSC  
buffer (0.3M NaCl and 0.003M sodium citrate) held in a  
35 S+S Minifold over one sheet of GB003 (S+S) filter



paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 $\mu$ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained  
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

## 6.2. RESULTS

### 10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells  
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 $\mu$ g/ml and 12.5ng/ml were tested for blockade of the  
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1<sub>LA1</sub>, HIV-1<sub>MAN</sub>, HIV-1<sub>RF</sub>, or HIV-1<sub>SF2</sub> virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection  
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV<sub>LA1</sub> inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study  
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 $\mu$ g/ml (FIG. 4). These observations  
35 indicate that the inhibitory effect of DP178 (SEQ



ID:1) is primary sequence-specific and not related to non-specific peptid /protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5       The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1<sub>SP2</sub> isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

10       The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).



### 6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4<sup>+</sup> CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1<sub>LAI</sub> isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 µg/ml) of peptide was incubated with 247 TCID<sub>50</sub> units of HIV-1<sub>LAI</sub> virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC<sub>50</sub>=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC<sub>50</sub> concentrations of approximately 5 µg/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1<sub>LAI</sub> or HIV-2<sub>NIH2</sub>. 62 TCID<sub>50</sub> HIV-1<sub>LAI</sub> or 25 GCID<sub>50</sub> HIV-2<sub>NIH2</sub> were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC<sub>50</sub> of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC<sub>50</sub> for HIV-2<sub>NIH2</sub>, thus making DP178 (SEQ ID:1) two logs more potent



as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

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7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

Approximately  $3.8 \times 10^5$  CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

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7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

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The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40µg/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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**TABLE XXIV**

5	Peptide	Peptide Concentration $\mu\text{g/ml}$	% Viability at time (hours)			
			0	24	48	72
10	DP178 (SEQ ID:1)	40	98	97	95	97
		10	98	97	98	98
		2.5	98	93	96	96
15	DP116 (SEQ ID:9)	40	98	95	98	97
		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

**8. EXAMPLE: THE INTERACTION OF DP178 AND DP107**

Soluble recombinant forms of gp41 used in the  
 example described below provide evidence that the  
 DP178 peptide associates with a distal site on gp41  
 whose interactive structure is influenced by the DP107  
 leucine zipper motif. A single mutation disrupting  
 the coiled-coil structure of the leucine zipper domain  
 transformed the soluble recombinant gp41 protein from  
 an inactive to an active inhibitor of HIV-1 fusion.  
 This transformation may result from liberation of the  
 potent DP178 domain from a molecular clasp with the  
 leucine zipper, DP107, determinant. The results also  
 indicate that the anti-HIV activity of various gp41  
 derivatives (peptides and recombinant proteins) may be



due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

### 8.1. MATERIALS AND METHODS

#### 5                   8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 10 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 15 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41Δ107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'- 20 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the 30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41- 35 PA178. All inserted sequences and mutated residues



wer checked by restriction enzyme analysis and confirmed by DNA sequencing.

#### 8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5       The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide  
10       gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,  
15       or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed  
20       protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

#### 25       8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells ( $7 \times 10^4$ ) were incubated with HIV-1<sub>MB</sub> chronically infected CEM cells  
30       ( $10^4$ ) in 96-well flat-bottomed half-area plates (Costar) in 100  $\mu$ l culture medium. Peptide and fusion proteins at various concentrations in 10  $\mu$ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated  
35       with microscopic examination. Both M41 and M41-P did



n t sh w cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO<sub>3</sub>, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H<sub>2</sub>O<sub>2</sub> were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H<sub>2</sub>SO<sub>4</sub> after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader



(Molecular Design) at 490 nm. Results are shown in FIG. 10.

## 8.2. RESULTS

### 8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

5           As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic  
10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because  
15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely  
20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind  
25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant  
30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix  
35 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein



eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

#### 8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic  
10 peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect  
15 HIV-1 induced membrane fusion at concentrations as high as 50  $\mu$ M (Table XXV, below).

**TABLE XXV**  
**DISRUPTION OF THE LEUCINE ZIPPER OF**  
**GP41 FREES THE ANTI-HIV MOTIF**

20		<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
	Cell fusion (IC <sub>50</sub> )	1 $\mu$ M	1 nM	> 50 $\mu$ M	83 nM	> 50 $\mu$ M
25	Fab-D binding (K <sub>D</sub> )	-	-	3.5x10 <sup>-9</sup>	2.5x10 <sup>-8</sup>	-
	HIV infectiv- ity (IC <sub>50</sub> )	1 $\mu$ M	80 nM	> 16 $\mu$ M	66 nM	> 8 $\mu$ M

30 1 The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

35 *Antiviral Infectivity Assays.* 20  $\mu$ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20  $\mu$ l of the indicated



concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20  $\mu$ l of CEM4 cells at  $6 \times 10^5$  cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO<sub>2</sub> incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID<sub>50</sub>) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

10

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1<sub>MB</sub> infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 $\Delta$ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

35



th DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs were tailored to the DP107 and DP178 sequences by



deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in  
 5 FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 10 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A  
 20 position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except  
 25 C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in  
 30 FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28  
 35 residues. FIG. 13 illustrates several possible



sequence alignments for both DP107 and DP178 and also includes motif d signs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.



Hybridizations can be performed in any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM



release 11.0). Of these, 1092 are viral enveloped r glycoprotein in sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein names and motif hit locations for all the motifs searched.

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10. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107 AND DP178-LIKE SEQUENCES IN HUMAN IMMUNODEFICIENCY VIRUS**

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV\_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV\_HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is



at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that  
 5 the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite  
 10 the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
 15 OF DP107-LIKE AND DP178-LIKE  
 SEQUENCES IN HUMAN RESPIRATORY  
SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF\_

20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with  
 25 similarities to DP-178, one just downstream of what would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids  
 30 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions  
 35 which share location similarities with DP-178 of HIV-1.



12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES  
IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name PENV\_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107-like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178 LIKE SEQUENCES  
IN CANINE DISTEMPER VIRUS

Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF\_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of



interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF\_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTIS finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTIS exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF\_p13H4;



(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits near the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68) at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTIS at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTIS predicted the greatest portion of the 88 residue stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

In the Example presented herein, respiratory syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated



that several of the identified peptides exhibit potential antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

#### 17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from  $A_{210}$  using Edlehoch's method (1967, Biochemistry 6:1948).

15

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

30

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

35



washed with DPBS (Dulbecco's Phosphate Buffered Saline w/ calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD<sub>450/690</sub> was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

**Peptides:** The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;



2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC<sub>50</sub> data for each peptide represents the average of several experiments conducted utilizing that peptide.

## 17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC<sub>50</sub> values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-



131, T-135 and T-137 to T-139, as demonstrated by their  $IC_{50}$  values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,  
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV  
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS  
TYPE 3 DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.  
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of  
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses  
35 consisted of circular dichroism (CD) studies. The CD



spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell in a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were  
5 determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPiV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to  
10 disrupt the ability of Hep2 cells chronically infected with HPiV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells  
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented  
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells  
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and  
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing  
35 uninfected CV-1W cells, then adding peptides (at the



dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50 $\mu$ l 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500 $\mu$ g/ml to approximately



500ng/ml. For each of the assays, a well containing no peptide was also used.

## 18.2 RESULTS

5 The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low  $IC_{50}$  values. In fact, peptides 201 to 205 exhibit  $IC_{50}$  values in the nanogram/ml  
20 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-  
25 HPIV3 antiviral compounds.

### 19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

30 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV\_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289.  
35 The peptide regions found by ALLMOTI5 were located at



amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN EPSTEIN-BARR  
VIRUS**

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB\_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results demonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located



at amino acid residues 193-220, as shown in FIG. 33. The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF\_MEASE), successfully identifying DP178/DP107 analogs.

10 The 107x178x4 motif identifies a single region at amino acid residues 228-262. The ALLMOTI5 search motif identifies three regions, including amino acid residues 116-184, 228-269 and 452-500. Three regions containing proline residues followed by a leucine zipper-like sequence were found beginning at proline  
15 residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface  
25 antigen precursor S protein were identified. The first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. The  
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral activity of these DP178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides  
35 represent one amino acid peptide "walks" through the



putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure at amino acids 424-459.

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24. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN BACTERIAL  
PROTEINS**

5 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

10 FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

15 FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

20 FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

25 FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The



region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues



55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS WITHIN VARIOUS  
HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.



26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107  
ANALOGS: CD AND ANTIVIRAL  
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum



[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50 µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.



The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.



The IC<sub>50</sub> values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35 µg/ml (T-257B1/C1) to 0.072 µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

5 Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10

27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS:  
ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides  
15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral  
20 capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis,  
25 A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk  
30 through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100 µg/ml to approximately 100 ng/ml. For each of the assays, a well containing no peptide was also used.

35



## 27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified  
10 viral peptide domains that represent highly promising anti-SIV antiviral compounds.

### 28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

#### 28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates.  
25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 30 1) FIGS. 49A-C present peptides derived from the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain  
35 truncations of this region and/or mutations



which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5           2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated  
10           in the figure.

Blocked peptides contained an acyl N-terminus and an amide C-terminus.

## 28.2 RESULTS

15           Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20           In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low  $IC_{50}$  values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50  
25           represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIH2 isolate demonstrated appreciable anti-HIV-2 antiviral  
30           activity.

35           Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ( $IC_{50} > 400 \mu\text{g/ml}$ ) whereas the carboxy terminal peptide showed potent antiviral



activity ( $IC_{50}$  = 3  $\mu$ g/ml). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and  
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the  
10 DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in FIG. 50 as T21) were also produced and tested, as shown  
15 in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by  
20 their low  $IC_{50}$  values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but  
25 truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107  
ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived  
30 from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-  
35 viral activity.



## 29.1 MATERIALS AND METHODS

### Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synth sized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a <sup>32</sup>P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.



## 29.2 RESULTS

Th EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects



f th inv ntion, and functionally equivalent methods  
and comp nents are within the sc pe of the invention.  
Indeed, various modificati ns f the invention, in  
addition to those shown and described herein will  
become apparent to those skilled in the art from the  
5 foregoing description and accompanying drawings. Such  
modifications are intended to fall within the scope of  
the appended claims.

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WHAT IS CLAIMED IS:

1. An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.  
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2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
3. The peptide of Claim 2 in which the virus is  
10 HIV-1 or HIV-2.
4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 15 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
6. The peptide of Claim 2 in which the virus is an influenza virus.  
20
7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
8. The peptide of Claim 2 wherein the virus is  
25 an Epstein-Barr virus.
9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide  
30 recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
10. The method of Claim 9 wherein the virus is  
35 HIV-1 or HIV-2.



11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

12. The method of Claim 9 wherein the virus is a human parainfluenza virus.

5

13. The method of Claim 9 wherein the virus is an influenza virus.

14. The method of Claim 9 in which the virus is a hepatitis B virus.

10

15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

15

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7872-020 (SHEET 1 OF 63)

HIV1LAI (DP-178; SEQ ID:1)	YTSLIHSLIEESQSQQEKNEQELLELDKWASLWNMF
HIV1SF2 (DP-185; SEQ ID:3)	YTNTIYNLLEESQSQQEKNEQELLELDKWASLWNMF
HIV1RF (SEQ ID:4)	YTGIIYNLLEESQSQQEKNEQELLELDKWANLWNMF
HIV1MN (SEQ ID:5)	YTSLIYSLLEKSQTQQEKNEQELLELDKWASLWNMF
HIV2ROD (SEQ ID:6)	LEANISKSLEQAQIQQEKINMYELOKLNWDIFGNMF
HIV2NIHZ (SEQ ID:7)	LEANISQSLEQAQIQQEKINMYELOKLNWDVFTNWIL
DP180 (SEQ ID:2)	SSSFILLEQNNHKLQLAEQMLEQINEKHYLEDIS
DP118 (SEQ ID:10)	QQLLDVWKRRQEMRLTVWGTKNLQARVTAIEKYLKDQ
DP125 (SEQ ID:8)	CGGNLLRAIEAQQHLLQLTVWG IKQLQARILAVERYLKDQ
DP116 (SEQ ID:9)	LQARILAVERYLKDQQQ

FIG.1



7872-020 (SHEET 2 OF 63)

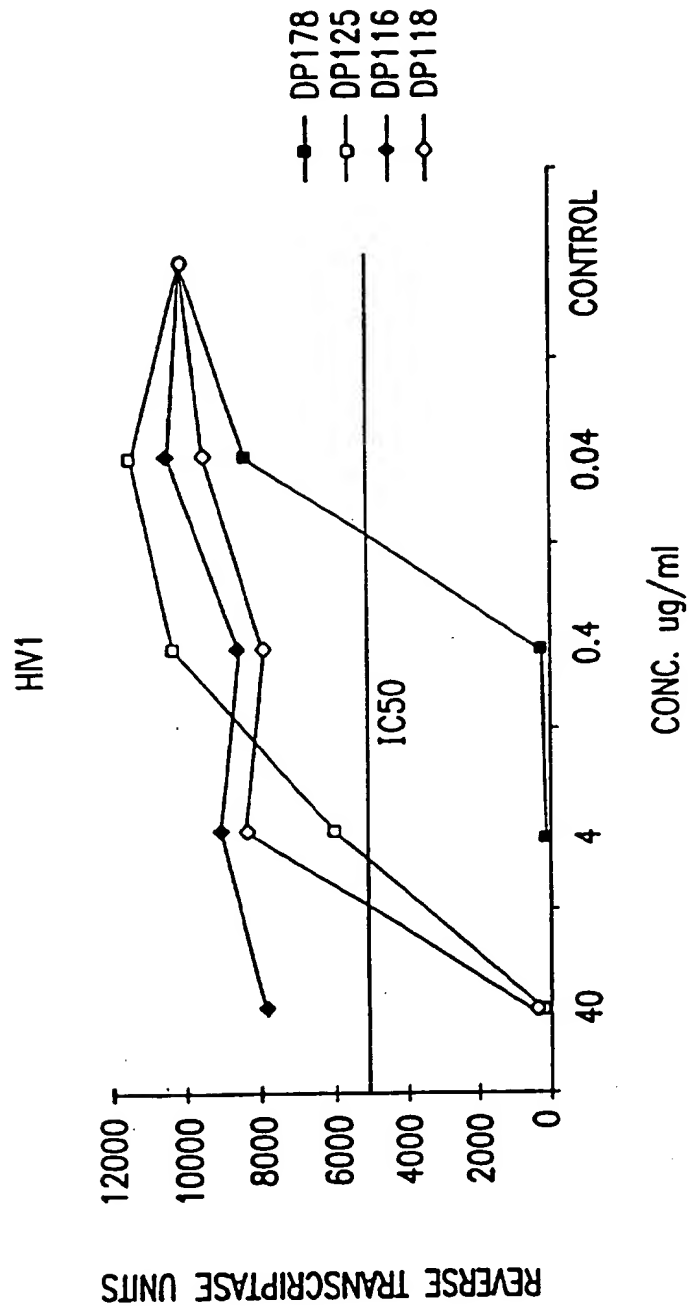


FIG.2



7872-020 (SHEET 3 OF 63)

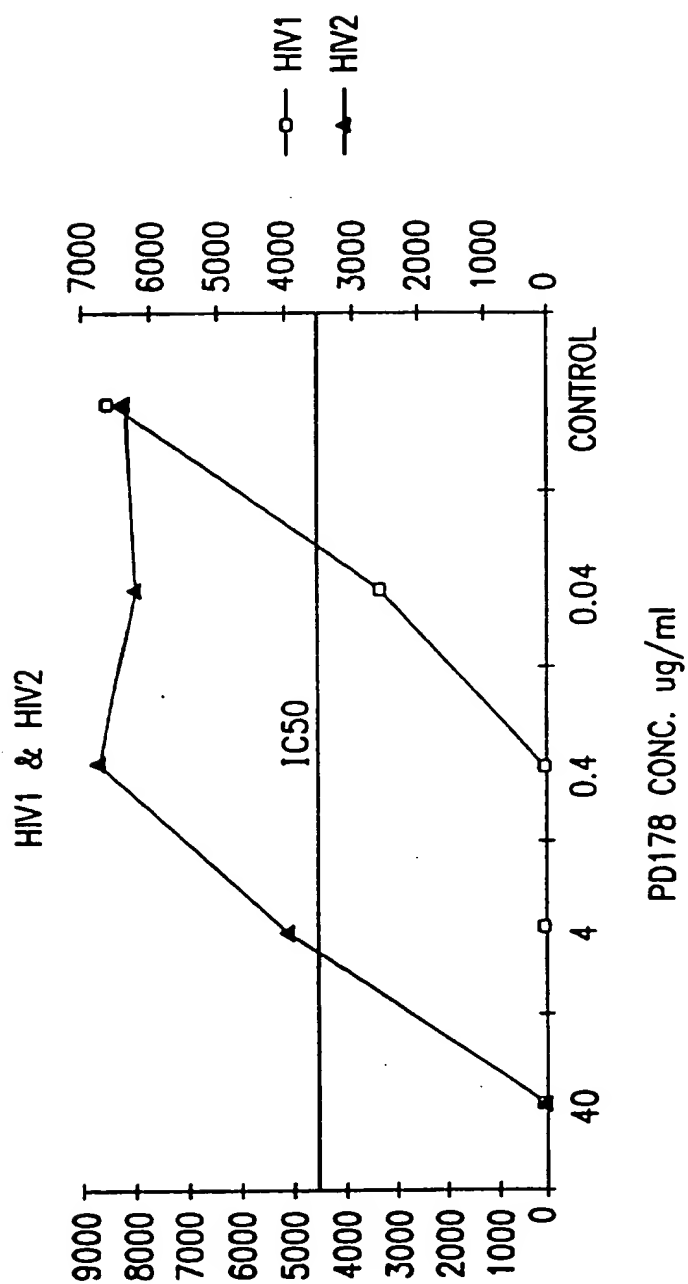


FIG.3



## 7872-020 (SHEET 4 OF 63)

Number of Syncytia/well: concentration in $\mu\text{g/ml}$ (micrograms/ml)									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LA1	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	0	0	0	0	0	ND	60

FIG.4B



## 7872-020 (SHEET 5 OF 63)

<u>HIV1</u>								
Number of Syncytia/well: concentration in ng/ml (nanograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV1</u>	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV1</u>	ND	48	ND	ND	ND	ND	ND	ND
<u>HIV2</u>								
Number of Syncytia/well: concentration in $\mu$ g/ml (micrograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV2</u>	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV2</u>	ND	58	ND	ND	ND	ND	ND	ND

FIG.5



7872-020 (SHEET 6 OF 63)

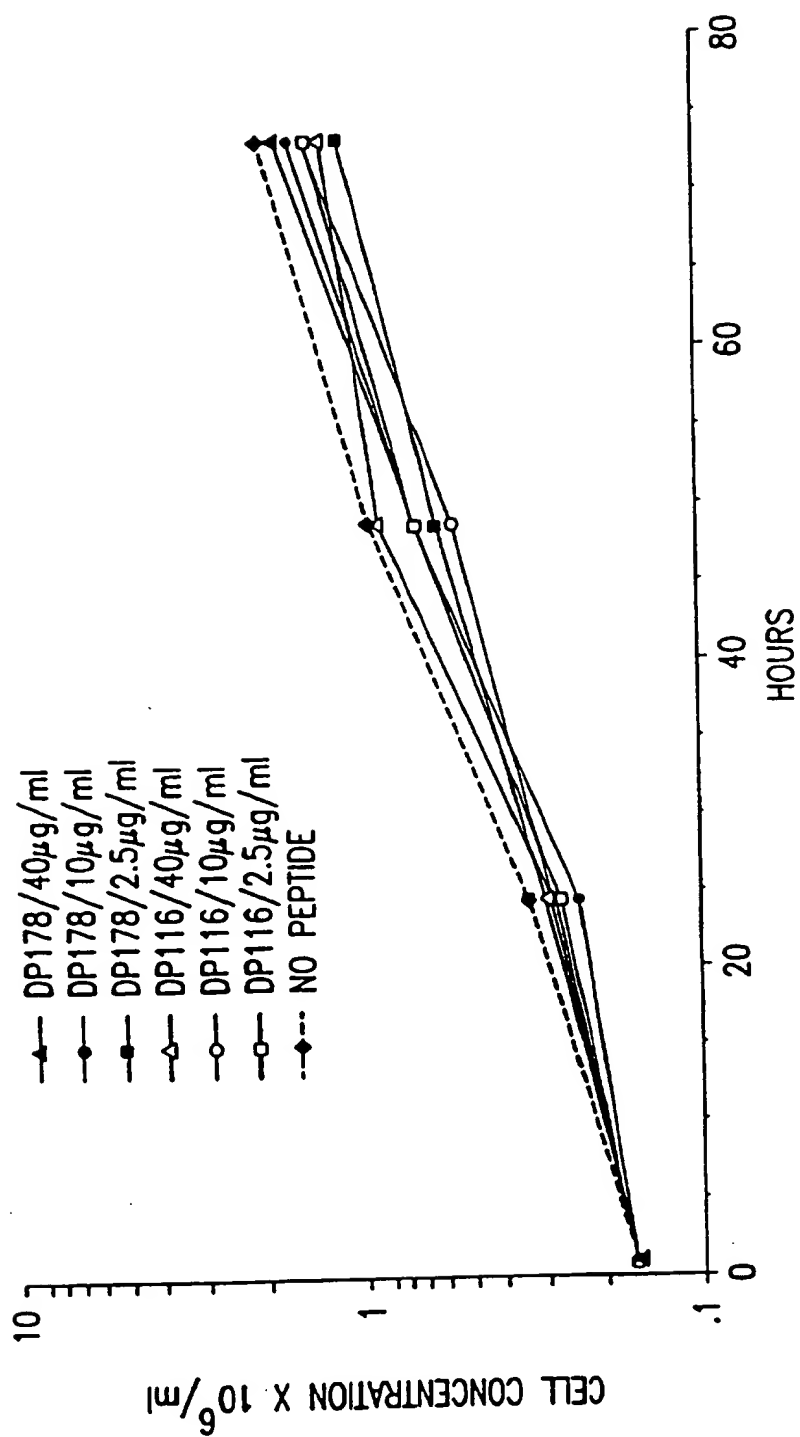


FIG.6



7872-020 (SHEET 7 OF 63)

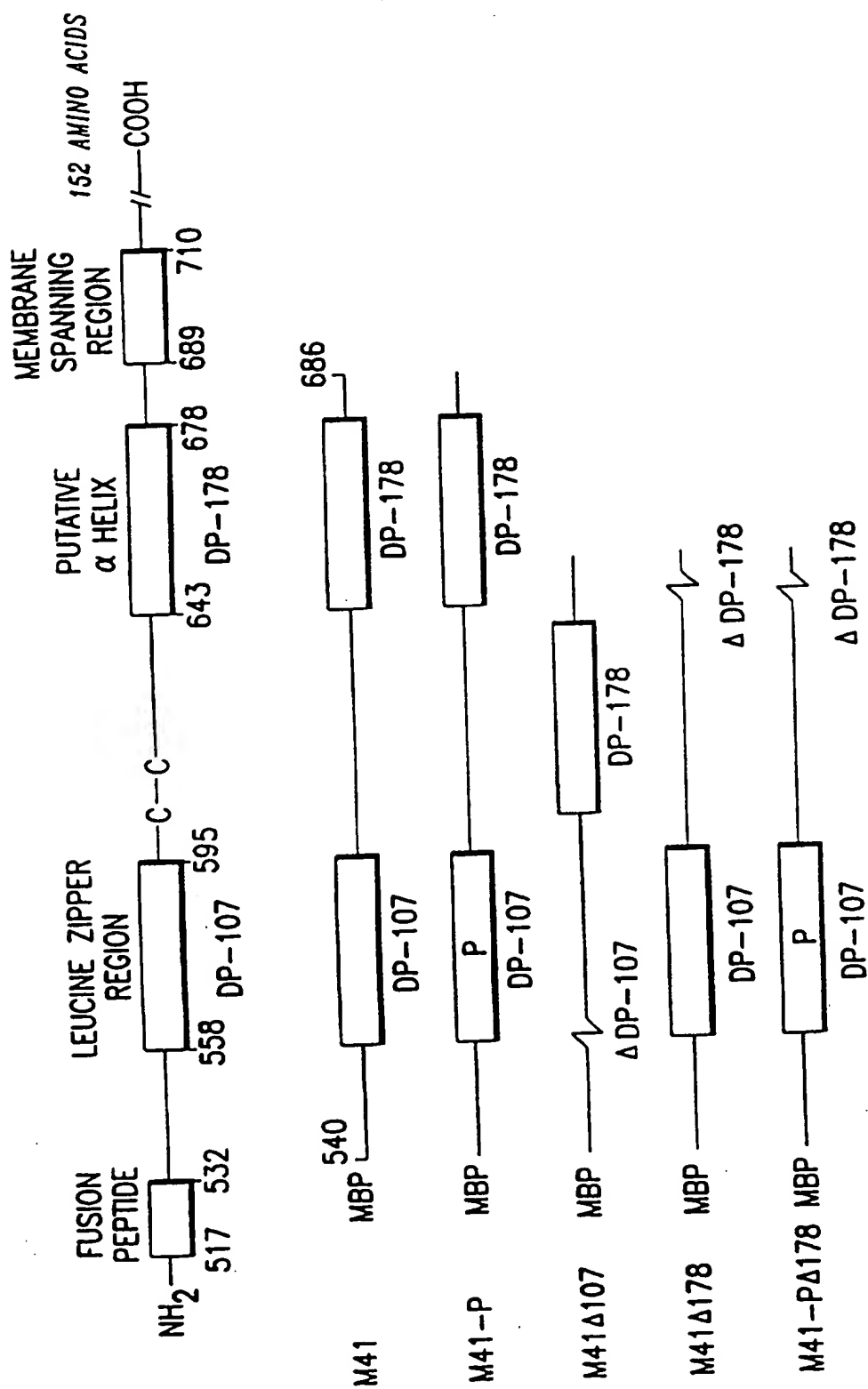


FIG.7



7872-020 (SHEET 8 OF 63)

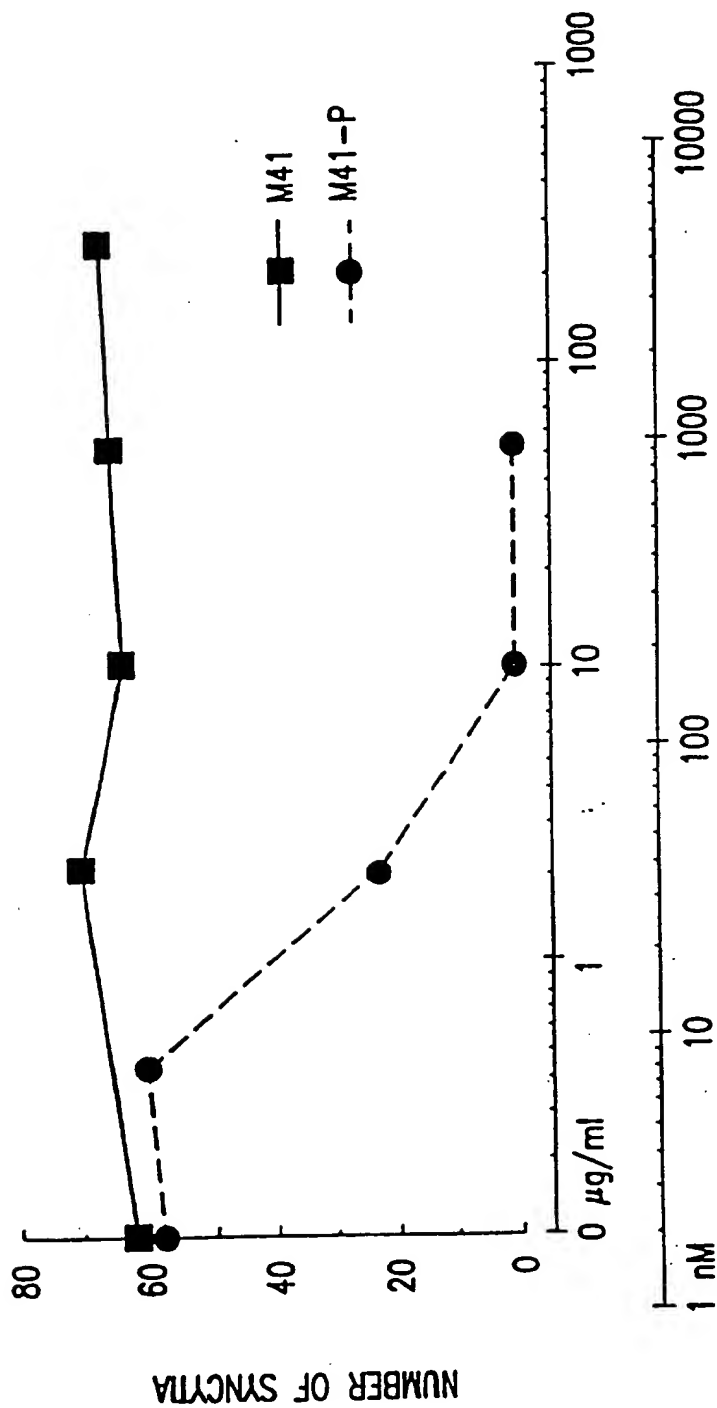


FIG. 8



7872-020 (SHEET 9 OF 63)

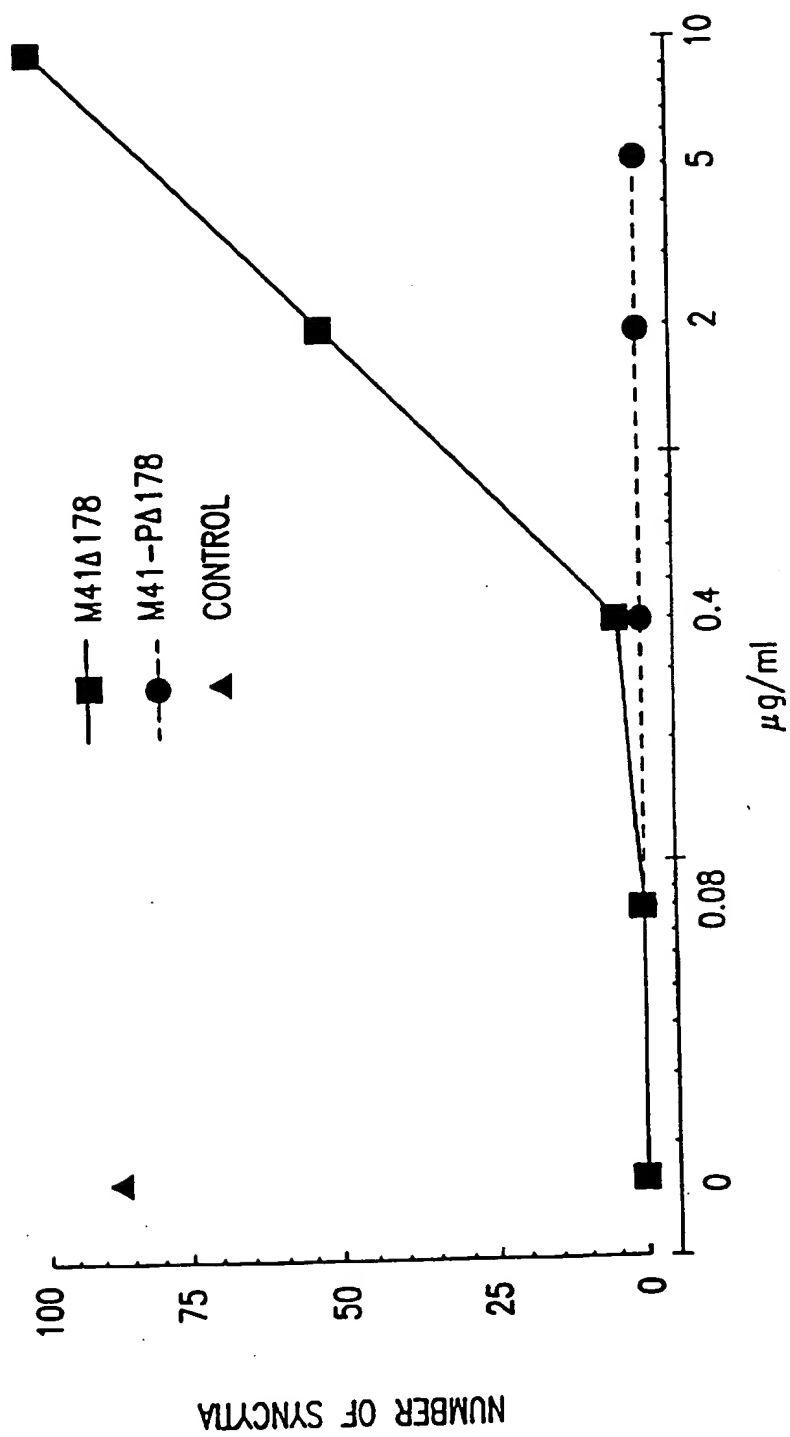


FIG.9



7872-020 (SHEET 10 OF 63)

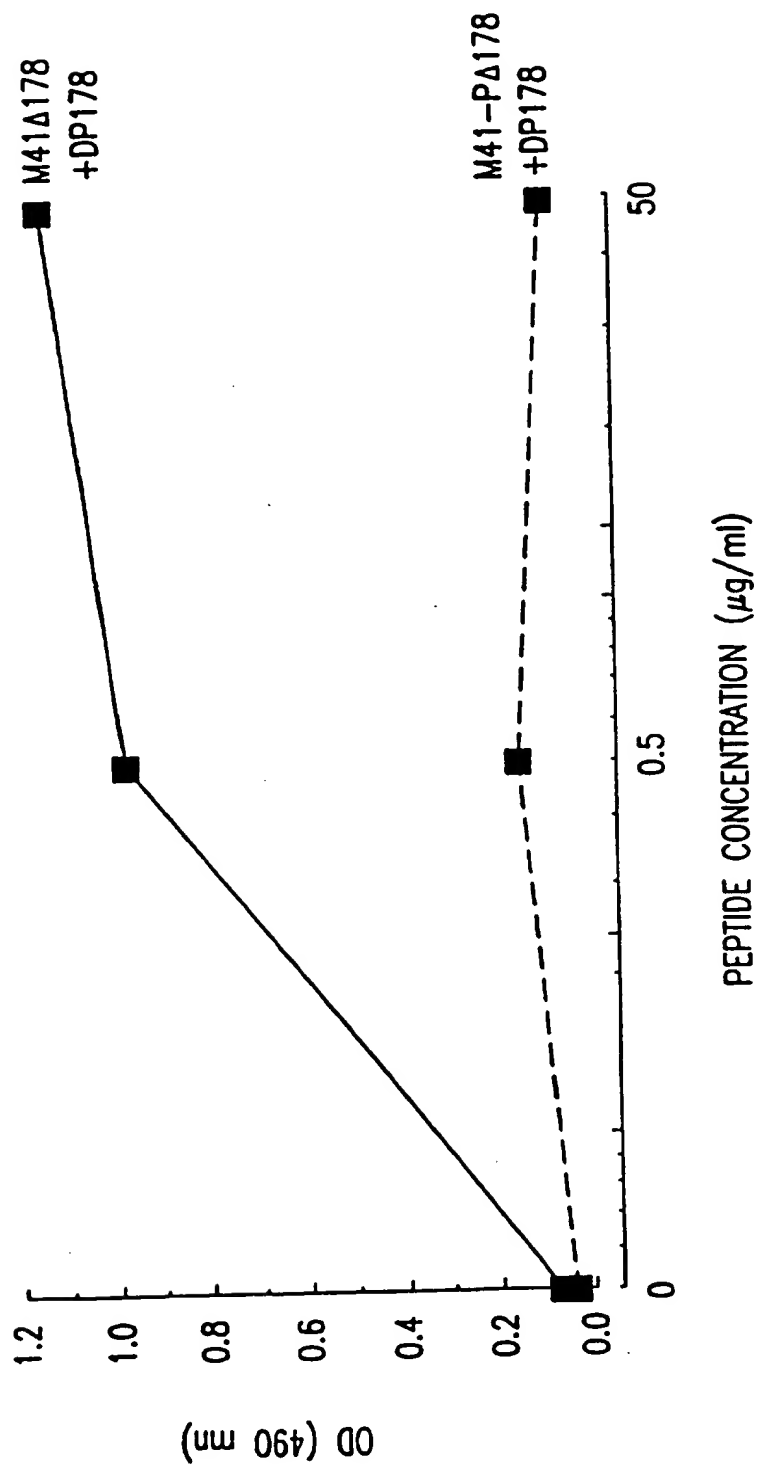


FIG.10



7872-020 (SHEET II OF 63)

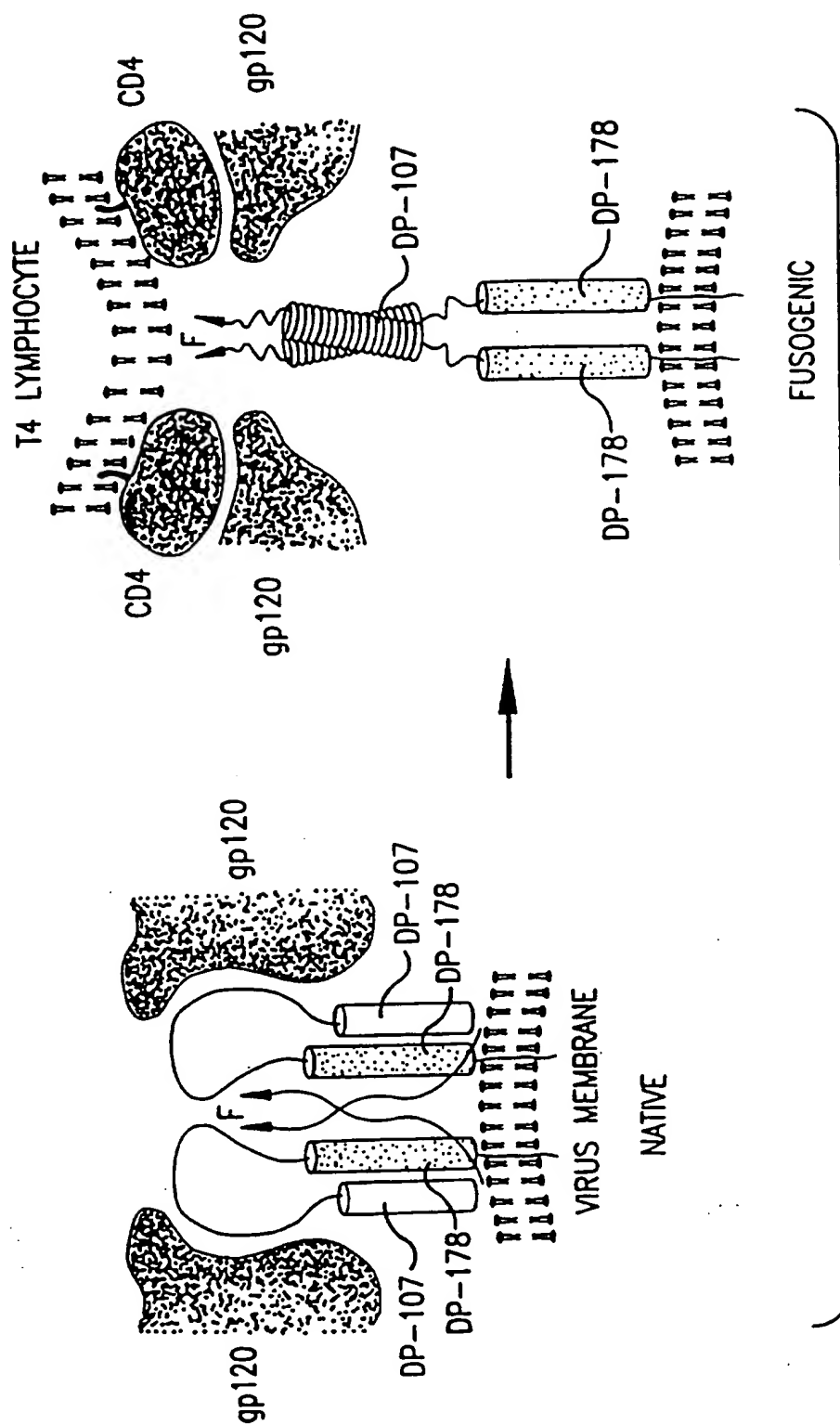
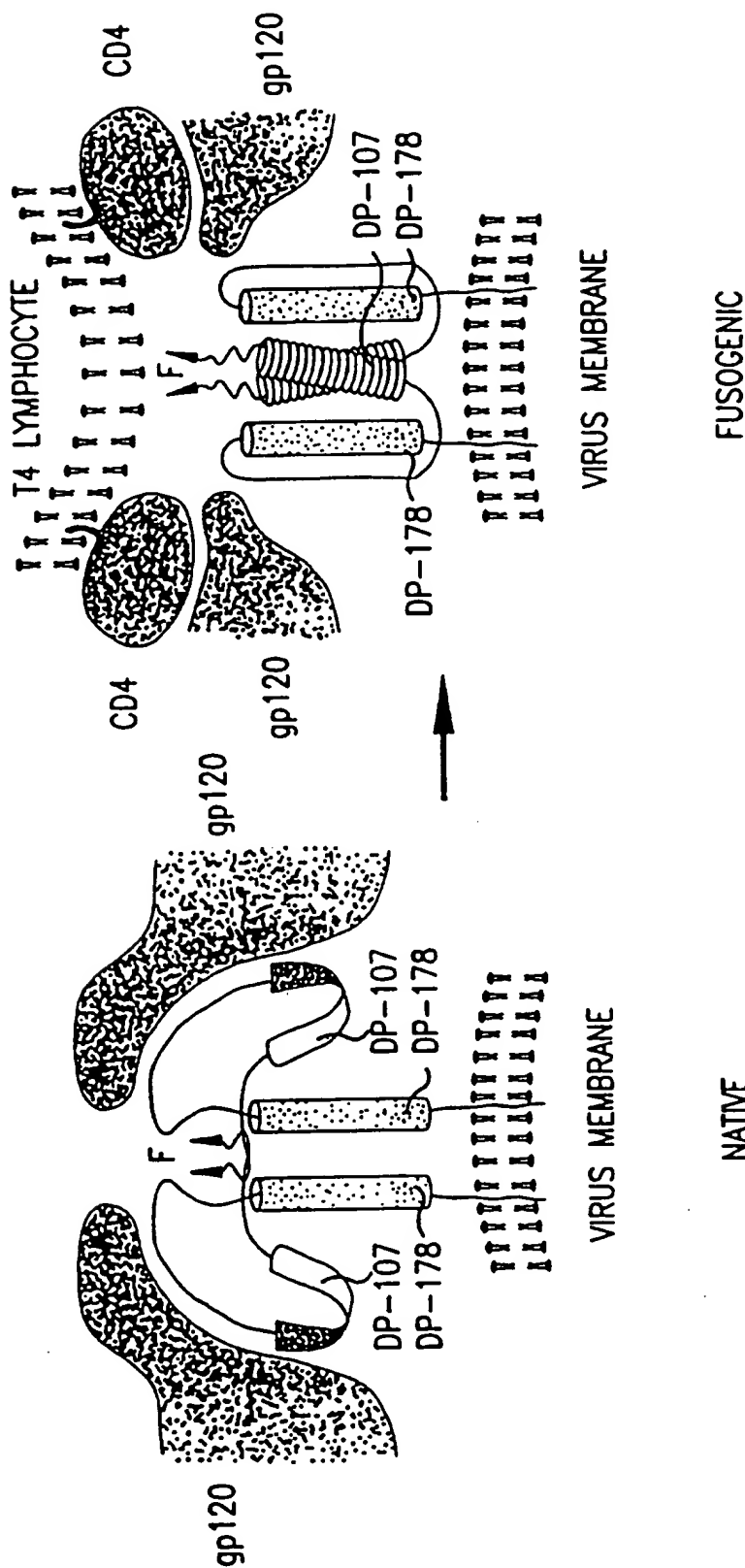


FIG.11A



7872-020 (SHEET 12 OF 63)

















7872-020 (SHEET 16 OF 63)

Sequence	Positions												Parent Motif	Hybrid Motif		
	A	D	A	D	A	D	A	D	A	D	A	D				
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	{LWNV} {CFGIMPWTW}	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EKLQVY} {ACFGMPRVWY}	{EKLQVY} {CFGMPW}
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EKLQVY} {CFGMPRVY}	{EKLQVY} {CFGMP}
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EFKLOVY} {CFGMPRVY}	{EFKLNQVWY} {CFGMP}
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EILNQSY} {ACFGMPRVWY}	{EILNQSVY} {CFGMPW}
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EILNQSY} {CFGMPRVY}	{EILNQSVWY} {CFGMP}
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EFILNQSY} {CFGMPRVY}	{EFILNQSVWY} {CFGMP}

FIG.15



7872-020 (SHEET 17 OF 63)

Sequence	Positions												Parent Motif	Hybrid Motif
	A	D	A	D	A	D	A	D	A	D	A	D		
DP-107 (env_hv1bru) L1=D	N	N	L	R	A	I	E	A	Q	H	L	L	[I L Q T V] {CDF I A P S T}	
DP-107 (env_hv1bru) L2=D	N	N	L	R	A	I	E	A	Q	H	L	L	[E K L N Q V] {CF K A P S}	
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	[E F K L Q W Y] {CF G A P R V Y}	
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	[E F L N Q S W Y] {CF G A P R V Y}	[E F I K L N Q S T W Y] {CF A P}
FLU LOOP 36	I	E	K	T	N	E	K	F	H	Q	I	E	[F I L T V] {A C F L A P T V H}	

FIG.16



7872-020 (SHEET 18 OF 63)

Sequence	Positions												Parent Motif	Hybrid Motif																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
GCN4 (gcn4 yeast)	A	D	A	D	A	D	A	D	A	D	A	D	[LMNV] {CFGIMP}TW																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
DP-107 (env_hv1bru)I1=D	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

FIG.17







7872-020 (SHEET 20 OF 63)

P-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(1)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(2)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(3)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(4)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(5)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(6)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(7)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(8)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(9)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(10)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-X(1,12)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-X(13,23)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]

FIG.19







## 7872-020 (SHEET 22 OF 63)

Fusion                      ♡ALLMOTIS♡  
 Peptide                      ♡107x178x4♡  
 ♡.....ELGEL      LGVGSALAS GVA      ♡YSKVLHLEGEVNIKSA

                                 ♡P1&12LZIPC♡  
LLSTNKAYVS LSNGVSVLTS KVLDLKNIYD KQ ♡ ♡LL ♡PIVNKQ

                 ♡107x178x4♡  
 SC ♡SISNIETVI ♡ EEQOKNNRLLLETTREESYNAG ♡ VTTT'VSTMLTNSSELLSL

                 ♡P1&12LZIPC♡  
                  ♡ALLMOTIS♡  
 INDM ♡PI ♡TNDQKKLMSNNVQI V ♡ RQQSYSI ♡ MS IKKEEVLAYV

VQ ♡ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

                 ♡P7, 12, & 23LZIPC♡  
                  ♡107x178x4♡                      ♡ALLMOTIS♡  
 EPIINFYDPLVF ♡PSDE ♡EDASISOVNEKINOSLAE ♡I ♡ RKSDELL ♡

                 ♡Transmembrane Region ♡  
HNVNA ♡ GK STTN ♡ IMITTIIVIVILLS LIAVGLLLY ♡ C ♡

KARSTPVTLS KDQLSGINNI AFSN

FIG. 21



## 7872-020 (SHEET 23 OF 63)

Fusion  
 Peptide      ♡ALLMOTIS♡      ♡107x178x4♡  
 .....FLGELG      ♡AAGTAMGAAA      ♡TALTVQSOHLLAGILOQOKNLLAAY

                 ♡107x178x4♡  
 EAQ♡ QQM ♡LKLTIWGYKNLNARVTALEKYLEDOARLN♡ AWG♡ CA

                                 ♡LVS Coiled-Coil♡  
                  ♡ALLMOTIS♡      ♡107x178x4♡  
 WKQVCHTTVP WQWNNRTPDW ♡NNMT ♡WLE ♡WEROISYLEGNTT

                                 ♡107x178x4♡  
 TOLEEARAQEEKNLD♡ AYOKLSS♡ WSDFWSW♡ FDF ♡SKWLN ♡ILK

♡Transmembrane Region♡  
IGELDVLGIGLRLLYTY♡ XS♡ CIARVRQGYSPSPQIHHP WKGPDPNAEG

PGEKGDKRKN SSEPWQKESG TAEWKS NWCK RL TNWCSISS IWL YNS

♡ALLMOTIS♡  
 ♡CLTL LVHLRSAFQY IQYGLGELKA AAQEA VVALA RLAQNAGYQIWL♡

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22



## 7872-020 (SHEET 24 OF 63)

Fusion ♣ 107x178x4 ♣  
 Peptide ♣ ALLMOTIS ♣ \*LVS Coiled-Coil\*  
 .....EAG ♣ VYL AGVALGVATA AQITAGIALHQ ♣ \*SNLNAQAIO

SLRTSLEQSNKAIEEIREATOETVIA \* VOGVODY ♣ VNNEl ♣ VP

♣ ALLMOTIS ♣  
 ♣ 107x178x4 ♣  
 ♣ P6 & 12LZIPC ♣

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD ♣ PISA ♣ ♣ EISIQALLYAL

GGEIHKILEKLGYSGSD ♣ MIALESRGIKTKI ♣ THVDLPGKF ILSISY

♣ P1 & 12LZIPC ♣  
 ♣ PTLSEVKGVIVHRLEAV ♣ SYNIGSQEWYTTVPRYIATNGYLISNFDDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYT

\*LVS Coiled-Coil\*  
 ♣ ALLMOTIS ♣  
 ♣ P12 & 23LZIPC ♣

DMVYEGKVAL G ♣ PAISLD ♣ RL \* DVGTNLGNALKKLD DAKVLI ♣

♦ Transmembrane Region ♦

DSS ♣ NOILETYR RS ♣ SFN ♦ EGSLLSVPILSCTAL ALLLLIYCC ♦

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

FIG. 23



## 7872-020 (SHEET 25 OF 63)

Fusion ♡ALLMOTIS♡  
 Peptide ♡107x178x4♡  
 ♡.....FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ♡ILRLKESITA  
  
TIEAVHEVTDGLSOLAYA ♡ VG KM♡ QQFVNDQFNNTAQELDCIKITQQV  
  
 ♡ALLMOTIS♡  
 GVELNLYLTELT TV FGPQITSPAL ♡TQLTIQALYNAGGNMDYLLTKLGVG  
  
 ♡P1 & 12LZIPC♡  
 NNQLSSLIGSGLIT GN♡ ♡PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET  
  
 LSVST TKGFASALVP KVVVTQVGSVI EELDTSYCIE TDL DLYCTRI VTFPMSPGIY  
  
 SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ  
  
 ♡ALLMOTIS♡  
 ♡107x178x4♡  
 NYGEAVSLID RHSCN ♡♡VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG  
  
 ♡LVS Coiled-Coil♡ ♡Trans-  
 ♡NLDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTSA ♡LIT ♡YLA  
  
membrane Region ♡  
LTAISLVCGII SLV ♡ ♡LACYLMY ♡ KQKAQQKTLLWLGNNTLGQMRATTKM

FIG. 24



## 7872-020 (SHEET 26 OF 63)

Fusion                      ♡ALLMOTIS♡  
 Peptide           ♡107x178x4♡    \*LVS Coiled-Coil\*  
 .....EEGGV    ♡IG ♡TIALG    \*VATSAQITA AVALVEAKOARSDIEKLKE

AIRDTNKAVOSVOSSIGNLIVAIKSVQ\* DYVNKE♡ ♡ IVPSIARLGCEAAG

♡ALLMOTIS♡  
 ♡107x178x4♡  
 LQLGIALTQH ♡♡YSELTNIEGDNIGSLOEKGKLOGIASLYRTNITE♡ ♡

♡P5 & 12LZIPC♡  
 IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL ♡PLLTRLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

♡ALLMOTIS♡  
 ♡107x178x4♡  
 ♡P6 & 23LZIPC♡  
 NDITLNNNSVALD ♡PIDI ♡SIELN ♡KAKSDLEESKEWI+ RRSNOKL÷

♡Transmembrane Region♡  
DSIGNWHQSSTT ♡IIIV ♡ LIM IILEIINVT II ♡ ILAVKYY ♡ R

IQKRNRVDQN DKPYVLTNK

FIG. 25



7872-020 (SHEET 27 OF 63)

Fusion  
Peptide  
.....GLEGAI AGFIENGWEGMIDGWYGFRRHQNSEGTG

♣107x178x4♣  
♥ALLMOTIS♥  
\*LVS Coiled-Coil\*  
\*Q ♥AADLKST ♣QAAIDQINGKLNRYIEKTEKTEHQIEKTESEVEGRIO

DLEKYYEDTKIDL\* WSYNAELLVALENOHTI♣ DLT♥ DSEMKNLFETR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

FIG. 26



7872-020 (SHEET 28 OF 63)

RSV F2	AV	Purified SCID (x.r.)	CD
T-143	++	39	++
T-143	++	31	++
T-144	+	114	++
T-144	++	40	+
T-148	+	281	+
T-148	+	204	+
T-147	+	354	+
T-148	+	336	+
T-148	+	342	+
T-148	+/	116	+
T-148	+/	117	+
T-148	+/	280	+
T-148	+/	118	+
T-148	+/	253	+

FIG. 27A



7872-020 (SHEET 29 OF 63)

[illegible]



7872-020 (SHEET 30 OF 63)

RSV DP-107-LIKE REGION (F1)		RSV		Position Assay		Position Assay	
RSV	DP-107	RSV	DP-107	AV	AV	Position Assay	Position Assay
T-100	T-100	T-100	T-100	204	204	204	204
T-101	T-101	T-101	T-101	319	319	319	319
T-102	T-102	T-102	T-102	326	326	326	326
T-103	T-103	T-103	T-103	34	34	34	34
T-104	T-104	T-104	T-104	80	80	80	80
T-105	T-105	T-105	T-105	80	80	80	80
T-106	T-106	T-106	T-106	209	209	209	209
T-107	T-107	T-107	T-107	343	343	343	343
T-108	T-108	T-108	T-108	177	177	177	177
T-109	T-109	T-109	T-109	118	118	118	118
T-110	T-110	T-110	T-110	372	372	372	372
T-111	T-111	T-111	T-111	307	307	307	307
T-112	T-112	T-112	T-112	187	187	187	187
T-113	T-113	T-113	T-113	60	60	60	60
T-114	T-114	T-114	T-114	194	194	194	194
T-115	T-115	T-115	T-115	99	99	99	99
T-116	T-116	T-116	T-116	18	18	18	18
T-117	T-117	T-117	T-117	86	86	86	86
T-118	T-118	T-118	T-118	160	160	160	160
T-119	T-119	T-119	T-119	204	204	204	204
T-120	T-120	T-120	T-120	44	44	44	44
T-121	T-121	T-121	T-121	44	44	44	44

FIG. 27 C



7872-020 (SHEET 31 OF 63)

RSV	Peptide #	AVG. IC <sub>50</sub> (XTT) ug/ml
T-12	VVSLSNQVSVLTSTSKVLDLKNYIDKQLL	>500
T-13	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-15	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-19	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-28	AGQVAVSKVLHLEGEVNNKIKSALLSTNKA VVSLSNQV	>500
T-28	AGQVAVSKVLHLEGEVNNKIKSALLSTNKA VVSLSNQV	327
T-30	VVHLEGEVNNKIKSALLSTNKA VVSLSNQVSVLTSTSK	328
T-68	VVSLSNQVSVLTSTSKVLDLKNYIDKQLL	292
T-70	VNKKIKSALLSTNKA VVSLSNQVSVLTSTSK	349
T-66	NDDQKKLMSNNVQIVRQQSYSIIMSIIEE	>500
T-576	SIENIEIVIEFQOKNNRLLLEITREFSVNAGVITPVIS	>100

FIG. 27D



7872-020 (SHEET 32 OF 63)

RSV DP-178-LIKE REGION (F1)										Fusion Assay									
RSV	T-47	F1-178	T-104	T-106	T-107	T-109	T-110	T-111	T-112	T-113	T-114	T-115	T-116	T-117	T-118	T-119	AV	Purified IC50 (log/ml) (XTT)	CD
																	++	17	++
																	+	95	
																	-	86	
																	++	20	
																	+++	8	
																	++	30	
																	+++	8	++
																	+++	6	++
																	+++	5	++
																	+++	9	++
																	+++	14	++
																	+++	5	++
																	+++	6	++

FIG. 28A







7872-020 (SHEET 34 OF 63)

HPV3 DP107-LIKE REGION (F1)																			



7872-020 (SHEET 35 OF 63)

HPV-3 DR107-Jha Waka		AVG. IC50	
T-42	A T B A G I T A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	943,000 ug/ml	
T-43	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	853,000 ug/ml	
T-39	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	720,000 ug/ml	
T-38	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	700,000 ug/ml	
T-40	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	54,788 ug/ml	
T-44	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	238,145 ug/ml	
T-45	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	488,000 ug/ml	
T-46	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	548,000 ug/ml	
T-582 Inactivated 104	L K E A I R D T N K A V Q S V Q S S I O N L I V A I K B	137,854 ug/ml	

29B



7872-020 (SHEET 36 OF 63)

PIN3 DP178-LIKE REGION 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MTRRRVLSVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSPFRVCELSSHGDLFRFSSD

♠107x178x4♠

IQCPSTGTRENTHEGLLMVFKDNIIPYSF ♠KVRSTKIVTNILYNGWYADSVTNRHE♠

EKFSVDSY ETDQMDTIYQ CYNVVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSSVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGLLLL AWLPLTPRSL ATVKNLTET TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPTTVMSSY GKAVAAKRLG DVISVSQCV VQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

♠107x178x4♠

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ♠SLIENIDFASLELYSRDEORASNVED ♠LE♠

\*LVS Predicted Coiled Coil\*

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVS\* GRNQ FVDGLGELMDSLGSVG QSITN

♠P12LZIPC♠

TM Potential

TM Potential

LVSTVGGLFSSLVSGFISF FK N ♠PFGGMLILVLVAGVVILVISL♠ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEATEF

FIG. 32



7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTPDYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQQQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@      ▲107x178x4▲    +Dimerization+  
@KRY KNRVASRKCRK ▲EK@ Q    +LLOHYREVAANKSSSENDRLRLLLKQ▲

MCPSLDVD+ SI IPRTDVLHE DLLNF

FIG. 33



## 7872-020 (SHEET 41 OF 63)

Fusion

Peptide

FAG

♥ALLMOTIS♥

\*LVS Coiled-Coil\*

♥VVLAGAALGVATAAQITAGIALHQSMLENSQAIDNLRASLETTN

QAIEAIRQAGQEMI\*LAVQGVQDYINN♥ ELIPSMNQLSCDLIGQKLGLKLLRYTT

♣P23LZIPC♣

♣P6,12LZIPC♣

♣107x178x4♣

♥ALLMOTIS♥

EILSLFGPSLRD ♣PISA ♣♥EISIQALSYALGGDINKV♣ LEKLGYSGGDL♣

♣P1,12LZIPC♣

LGILES♣ RGIKARI♥ THVDTESYFIVLSIAY ♣PTLSEIKGVTVHRLEGV♣ SY

NIGSQEWYTTVPKYVATQGYLISNFDDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

♣P23LZIPC♣

♣P12LZIPC♣

♥ALLMOTIS♥

\*LVS Coiled-Coil\*

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS\*LERLDVGTNLGN

♦Transmembrane Region♦

AIAKLEDAKELL♣ ESSDOI\*L♣ RSMK ♦GLSSTSIVYILI♥ AVCLGGLIGIPALICCC♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRS

FIG. 34



## 7872-020 (SHEET 42 OF 63)

## Pre S1 and Pre S2

MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG  
 LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM  
 QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRI GDPALN

## Major Surface Antigen (HBs)

Fusion

Peptide

✦P12 &amp; 23LZIPC✦

MENITSG FLG ✦PLL VLQAGFFLLTRILTI✦ PQSLDSWWTSLNFLGGTTVCLG

✦P12 &amp; 23LZIPC✦

QNSQSPTSNHSPTSCPPTC ✦PGYRWMCLRRFIIFLLCLIFLLVLLDYQGML✦

PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

✦Transmembrane Region✦LWEWASARFSWLS ✦LLVPFVQWFVGLSPTVWLSVI✦ WMMWYWGPSL✦Transmembrane Region✦✦YSILSPELPLLPIEFCLWVYI✦

FIG. 35



## 7872-020 (SHEET 43 OF 63)

Fusion ♥ALLMOTI5♥ ♠107x178x4♠  
Peptide \*LVS Coiled Coil  
AIQLIPLFVG LGI ♥TTAVSTGAAGLGVS ♠IT \*QYTKLSHQLISDV

QAISSTIQDLQDOVDSLAEVVLO\* NRRGLDLLTAE♠ QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....????????????????????????????????.....

FIG 36



7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

♠107x178x4♠

♥ALLMOTIS♥

♠♥YQDYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA♠ T♥

PK DTQYDIGFT

♠107x178x4♠

♥ALLMOTIS♥

♠♥ESTLLDGSQKSGKSIQVTDNODGTVELVATLGKSSGS♠ AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

FIG. 37



7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

♠107x178x4♠

♥ALLMOTI5♥

♠♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTTAT♠

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38



7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

♠107x178x4♠

♥ALLMOTIS♥

♠♥SWKNVDKENNETLKNEOTTADYATNVNI♠

QLMESNGTKAISVVGKETE♥

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

FIG. 39



7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLLATT ATDFTPVP

♠107x178x4♠

♥ALLMOTIS♥

♠♥LSSNOIHK TAKASTNDNIKDLLDWYSSGSDTETNS♠♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

♠107x178x4♠

♠DLNTRTKKSOHTSEGTYIHEQISGVT♠

NTEKLPTPIEL PLKVKVHVKD SPLKYG

♣P12LZIPC♣

♣PKFDKKQLAISTLDFEIRHQLTQI♣

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40



7872-020 (SHEET 48 OF 63)

♥ALLMOTIS♥

MKKTAFILLL FIALTLTTSP L ♥VNG

♠107x178x4♠

\*LVS Predicted Coiled-Coil\*

\*S ♠EKSEEINEKDLRKKSELORNALSNLROIY\* YYNEKAITENKESDD♠

QFLENTLL♥ FKG FFTGHPW

♠107x178x4♠

♠YNDLLVDLGSKDATNKYKGKKVDLYGAY♠

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEKKVP INLWIDGKQTTV

♣P12LZIPC♣

♣PIDKVKTSKKEVTVQELDL♣ QARHYLHGK FGLYNSDSFGGKVQ

♣P12LZIPC♣

RGLIVF HSSEGSTVSY DLFDAQGQY ♣P DTLLRIYRDN KTINSENLHI♣

DLYLYTT

FIG. 41



7872-020 (SHEET 49 OF 63)

♥ALLMOTIS♥  
 ♥VNGS  
 MKKTAFTLLL FIALTLTTSP L

♠107x178x4♠

♠EKSEEINEKDLRKKSELOGTALGNLKOYYYNEKAKTENKESHDA Q♥

FLQHTILFKG FFTDHSWYN̄D LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

♠107x178x4♠

♥ALLMOTIS♥

♣P12LZIPC♣

♣P ♥L ♠ETVKTNNKNVTVOELDLOARRYL♣ QEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

♣P23LZIPC♣

♣PSVNYDLFGAQQQYSNTLLRIYRDNKTINSENMI♣ DIYLYTS

FIG. 42



7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

♥ALLMOTIS♥

♥QMNNLYDHARGTQTGFVRYDDGYV

♠107x178x4♠

♠STSLSLRSAHLA GOYILSGYSLTIYIVI♠ ANMFNVNDVISVY♥

SP HPYEQEVSA L GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ALLMOTIS♥

♥ETQNLSTIYLR EYQSKVKRQIFSDYQSEVDIYNRI RDEL♥

FIG. 43



7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSTYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWL VQPA

LVSSVAPSQT RAPHFPGVPA PSAGAYS RAG VVKMTGGRA

\*LVS Predicted Coiled-Coil\*

QSIGRRGKVE QLSPEEEKR RIRRE \*RNKMA AAK

♠ 107x178x4 ♠

♥ ALLMOTIS ♥

♥ CRNRRREL ♠ TDTLQAETDOLEDEKSALQTEIANLLKEKEKL ♥

EFILAAH R\* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARVP

DMDLSGSFYA GSSSNPSSD SLSSPTLLAL

FIG. 44



7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDDEEAEQEEENLEASGDYKYSGRDSLIFLVDASKA  
 MFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNS  
 VNFKNITYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY  
 SLSEVLWVCANLFSVDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR  
 TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

♠107x178x4♠

♥ALLMOTIS♥

\*LVS Predicted Coiled-Coil\*

♥LRVH \*FEE ♠SSKLEDLLRKVRKETRKRALSRLKLNKDIV\* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE  
 ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK  
 IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS  
 DSFENPVLQQHFRNLEALALDLME

♣P12LZIPC♣

♣PEQAVDLTLPKVEAMNKRL♣ GSLVDEFKELVYPPDYNPEGKVTKR

KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG

LKKQELLEALTKHFQD

FIG. 45



## 7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♠107x178x4♠

♥ALLMOTI5♥

♥♠LTAWSRTLVTFKDVEVDEFTREEWKLLDT♠ AQQIVYRNV

MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD  
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR  
DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT  
HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH  
SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVVRPYECN  
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSSRSHLYSHQRT  
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN  
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♣P23LZIPC♣

♣PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♣ RENAY

FIG. 46



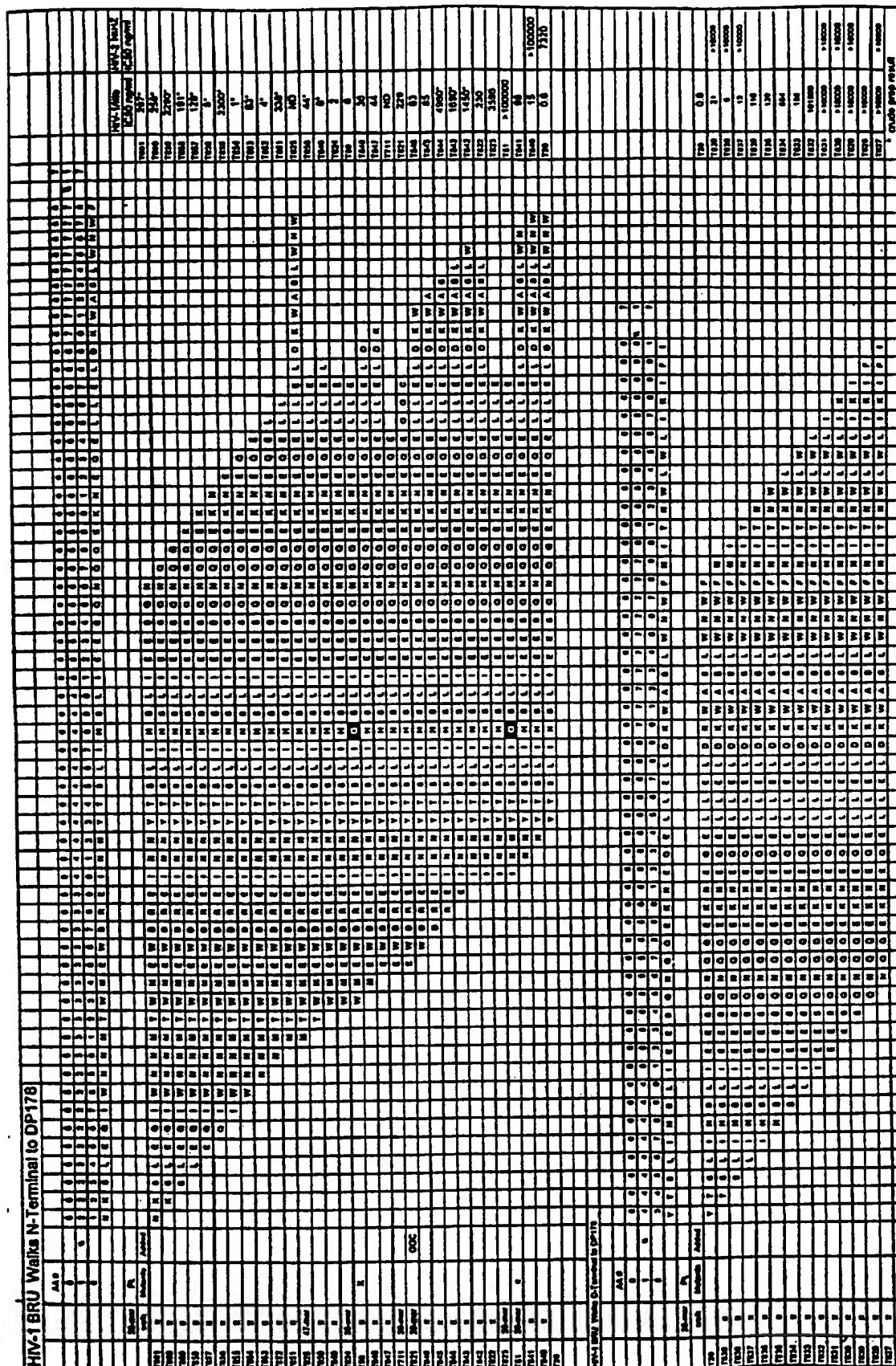








7872-020 (SHEET 56 OF 63)



ETC 49A



# 7872-020 (SHEET 57 OF 63)

HIV-1 Brd 178 Constructs, Mutations, Truncations									
Construct	Position	Sequence	Notes	Read	Read	Read	Read	Read	Read
16	178	ATG							
17	178	ATG							
18	178	ATG							
19	178	ATG							
20	178	ATG							
21	178	ATG							
22	178	ATG							
23	178	ATG							
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26	178	ATG							
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37	178	ATG							
38	178	ATG							
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42	178	ATG							
43	178	ATG							
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45	178	ATG							
46	178	ATG							
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48	178	ATG							
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122	178	ATG							
123	178	ATG							
124	178	ATG							
125	178	ATG							
126	178	ATG							
127	178	ATG							

Fig. 49B



## 7872-020 (SHEET 58 OF 63)

HIV-1 Bru 178 Constructs, 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Readline	173	B	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	219	ACT	Rea	
T-421	173	B	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	208	+	35
T-422	174	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	209	+	35
T-423	175	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	210	+	35
T-424	176	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	211	+	35
T-425	177	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	212	+	35
T-426	178	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	213	+	35
T-427	179	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	214	+	35
T-428	180	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	215	+	35
T-429	181	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	216	+	35
T-430	182	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	217	+	35
T-431	183	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	218	+	35
T-432	184	E	E	I	E	I	K	R	Y	K	N	R	V	A	S	R	K	G	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	A	K	S	E	N	D	R	L	R	L	L	L	219	+	35
T-433																																																		
T-434																																																		
																																													</					



7872-020 (SHEET 61 OF 63)

Residue	197	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		46
T-447	197	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		232		36
T-448	198	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		233		36
T-449	199	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		234		36
T-450	200	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		235		36
T-451	201	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		236		36
T-452	202	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		237		36
T-453	203	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		238		36
T-454	204	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		239		36
T-455	205	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		240		36
T-456	206	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		241		36
T-457	207	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		36
T-458	208	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		243		36
Residue	209	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F								246		37	
T-459	209	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F								244		36	
T-460	210	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F								245		36	
T-461	211	S	E	N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F								246		36	

FIG. 51B



## 7872-020 (SHEET 62 OF 63)

## Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T  
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T  
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V  
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C  
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L  
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G  
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q  
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N  
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S  
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q  
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

I=I6. 52A



7872-020 (SHEET 63 OF 63)

Domain II:  
223P.G.Y.R.W.M.C.L.R.F.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.G.S.S.T.S.T.G.P.C.R.T.C.M.T.T281

P.O.Y.R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L  
G.Y.R.W.M.C.L.R.R.P.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P  
Y.R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V  
R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C  
W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P  
N.C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L  
C.L.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I  
L.R.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O  
R.R.R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S  
R.F.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S  
P.I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S  
I.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T  
I.F.L.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S  
P.L.F.I.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T  
L.F.I.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O  
F.I.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P  
I.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C  
L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R  
L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T  
L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C  
C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M  
L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M.T  
I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M.T.T

P-26. 52 B



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US95/16733**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C07K 7/04, 14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/99

US CL : 530/324; 424/184.1

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1, 186.1, 187.1, 188.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, AIDSLINE, APS

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 89, Number 21, issued November 1992, Wild et al, "A Synthetic Peptide Inhibitor of Human Immunodeficiency Virus Replication: Correlation Between Solution Structure and Viral Inhibition", pages 10537-41, see entire document.	1-3, 9, and 10 ----- 4-8 and 11-15

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

28 MARCH 1996

Date of mailing of the international search report

09 APR 1996

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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US95/16733

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 ----- 4-8 and 11-15
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4 ----- 9 and 11
X ----- Y	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 5 ----- 9 and 12
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	1 and 6 ----- 9 and 13
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 ----- 9 and 14
P, Y	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15